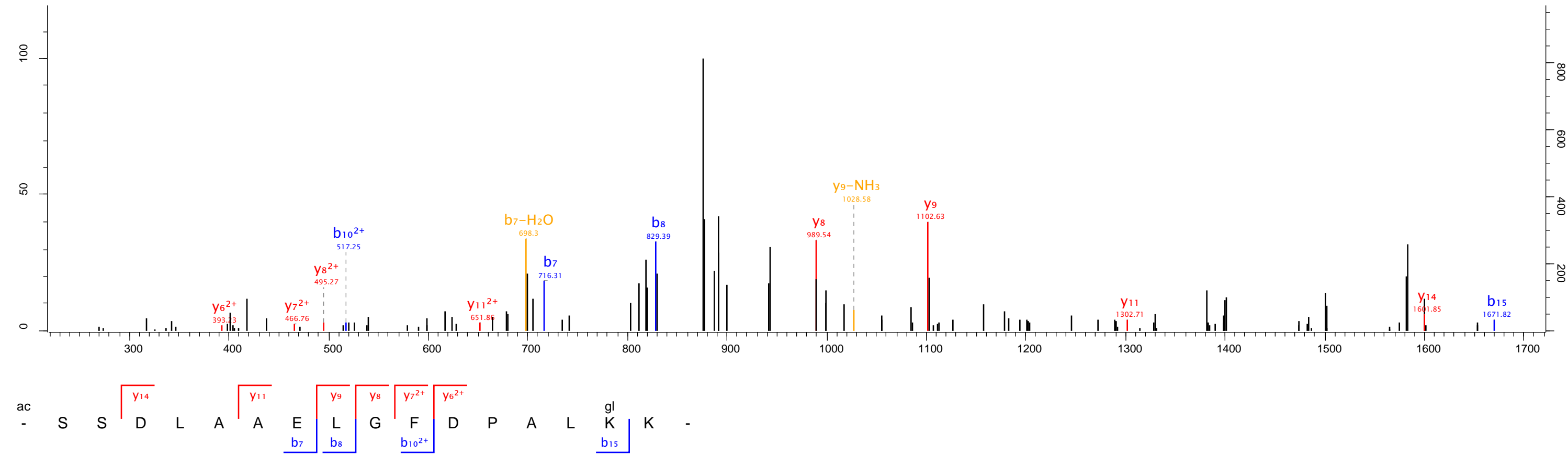
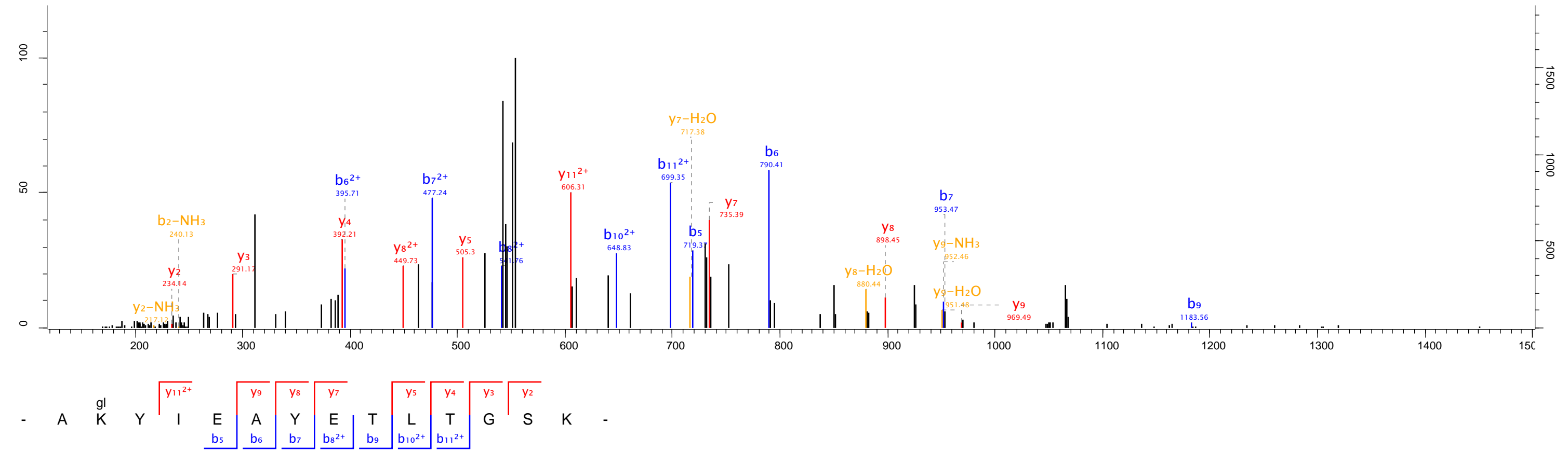


Raw file
tay_Yeast_Untreated_WCLip_GG_CID_01August14_04

Scan	Method	Score	m/z
14254	ITMS; CID	62.68	909.97

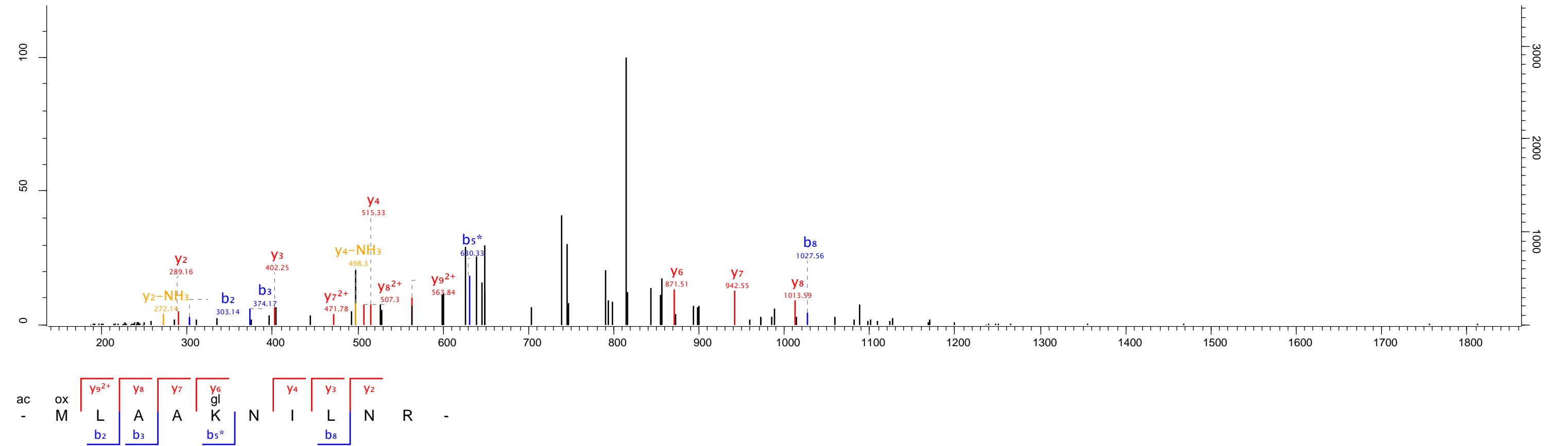


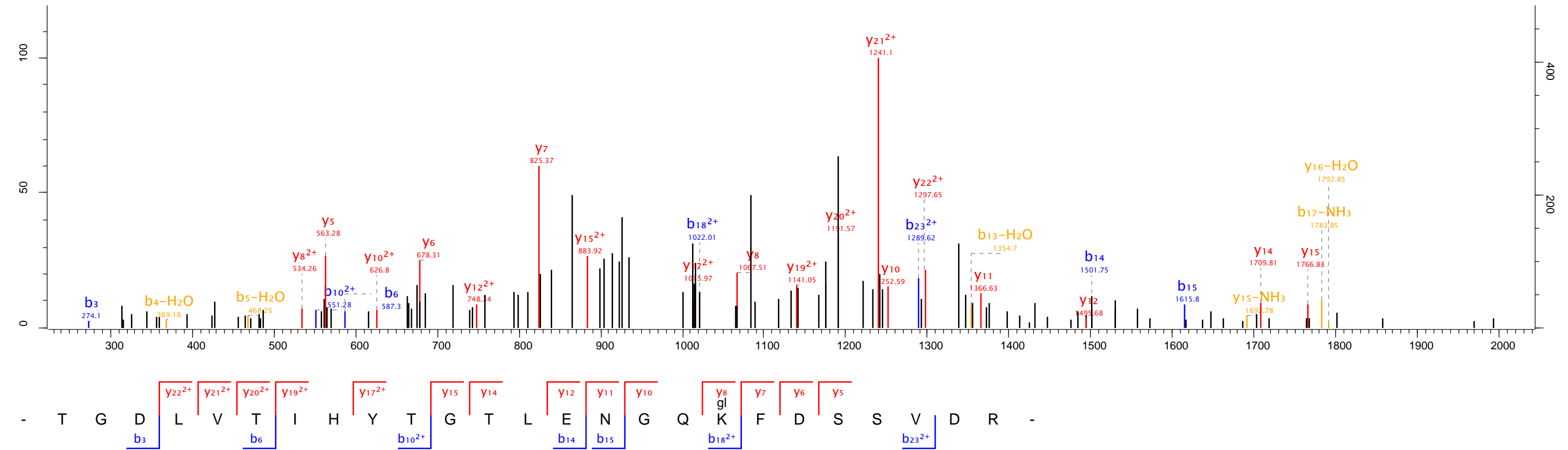


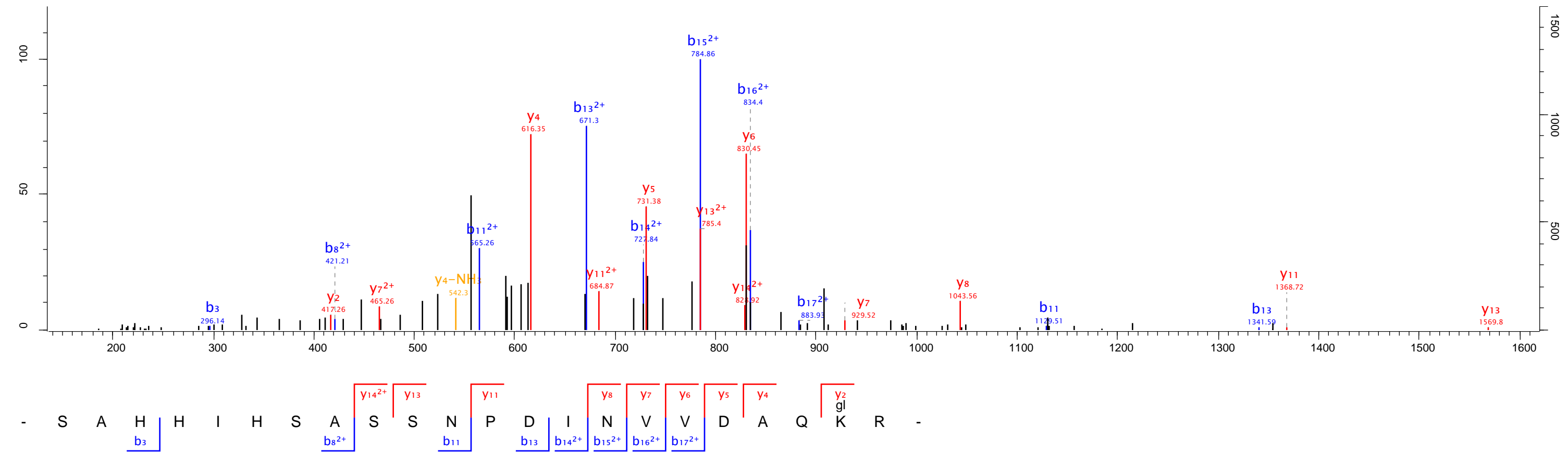
Raw file

ScanMethodScorem/z

tay_Yeast_Untreated_WCLip_GG_CID_01August14_0415744ITMS; CID86.67658.55

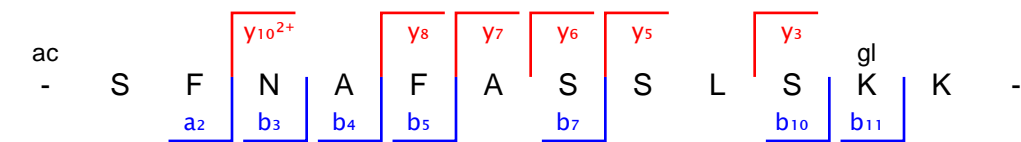
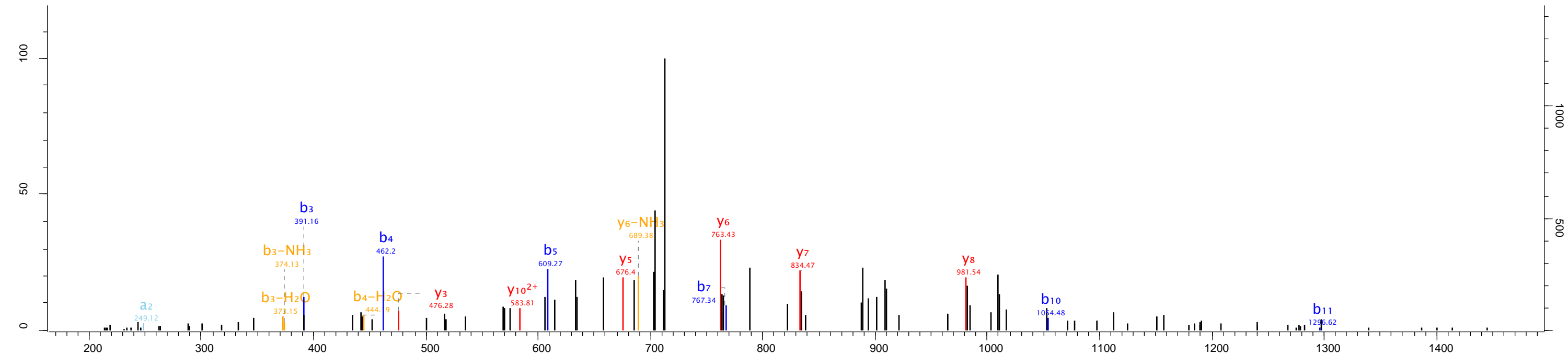


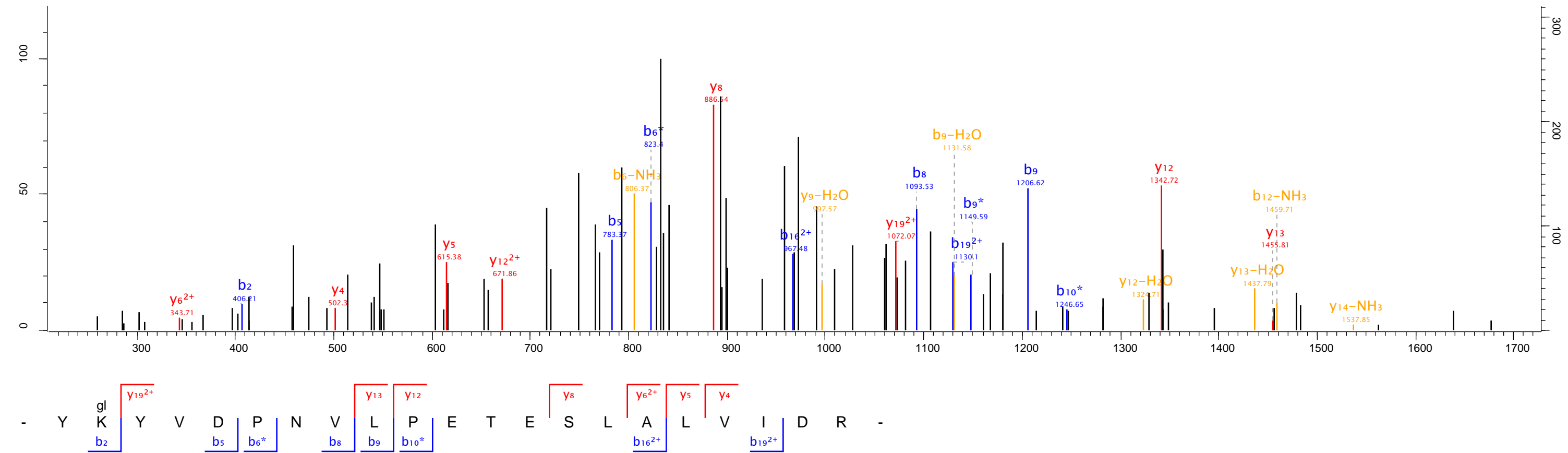


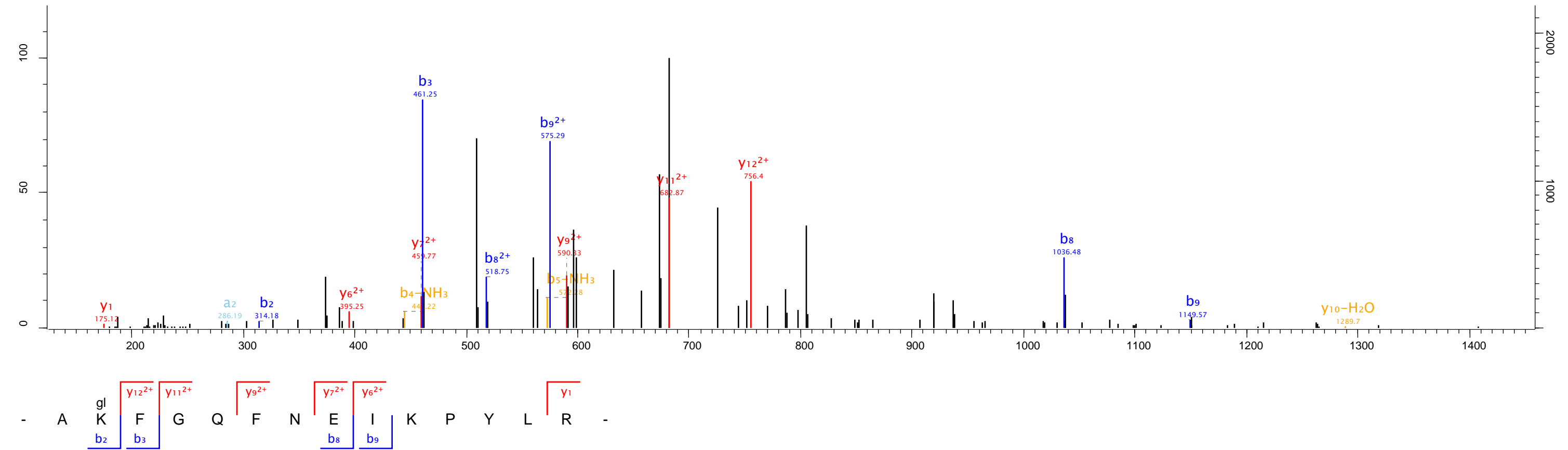


Raw file
tay_Yeast_Untreated_WCLip_GG_CID_01August14_04

Scan	Method	Score	m/z
22475	ITMS; CID	57.43	722.34

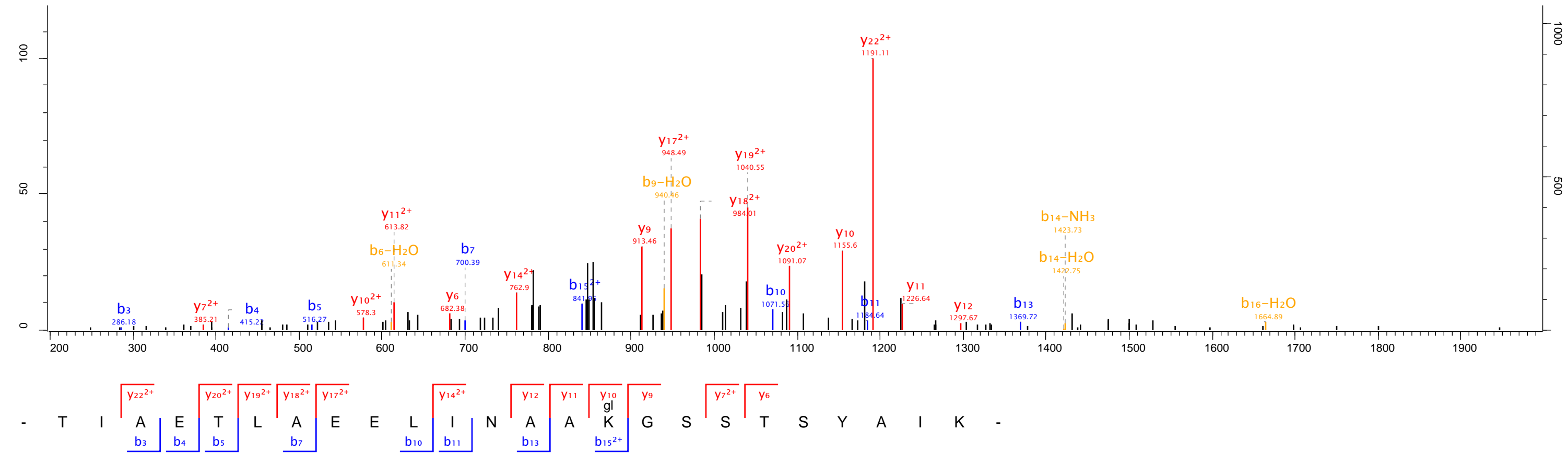


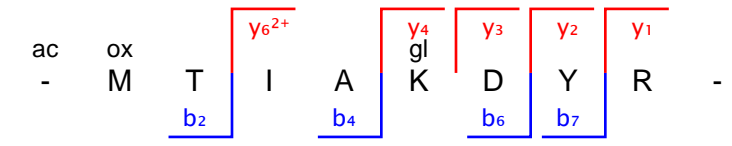
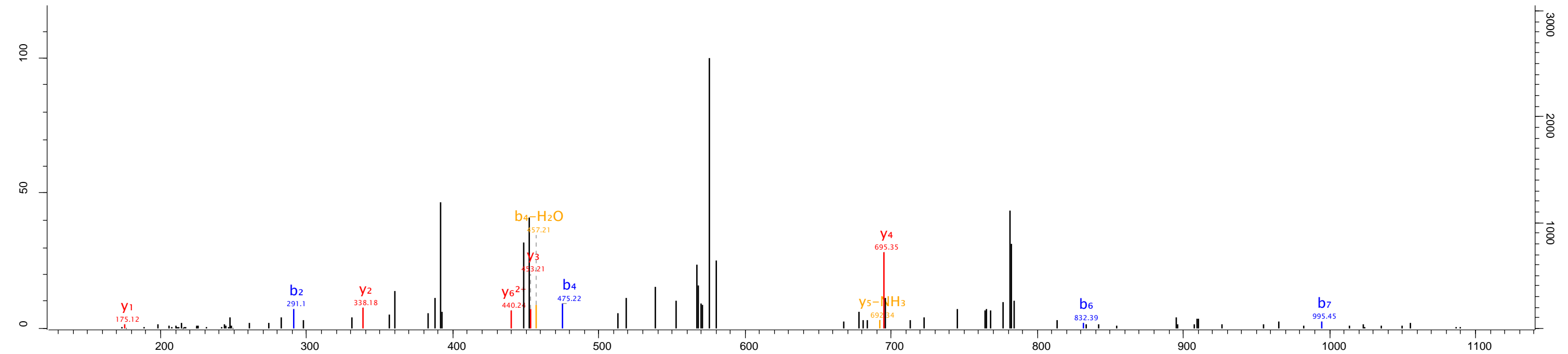


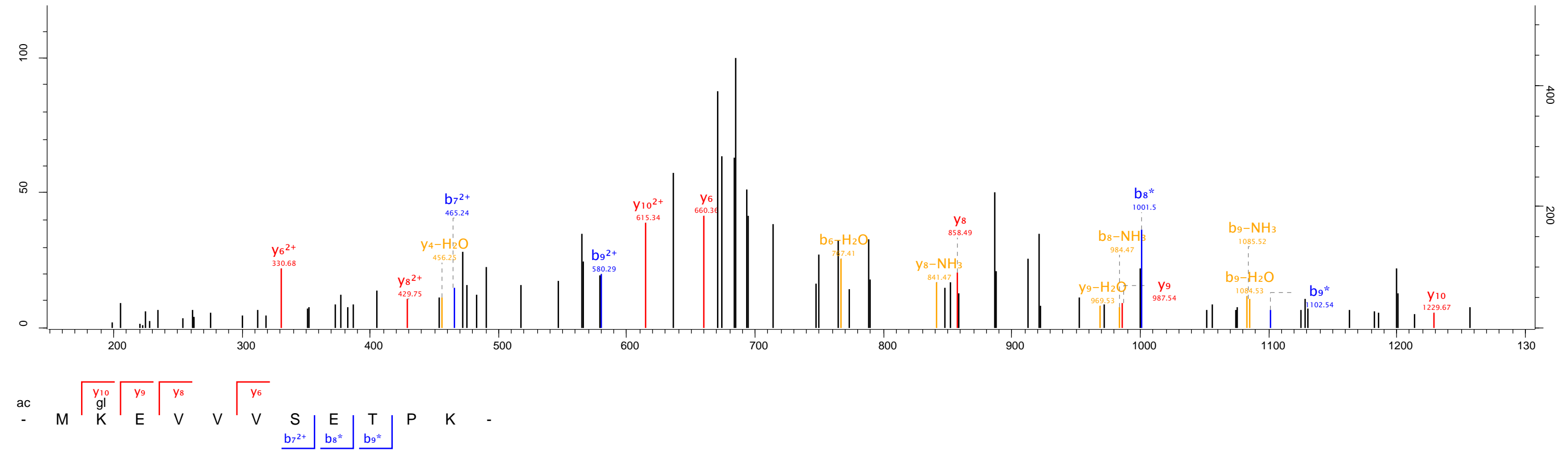


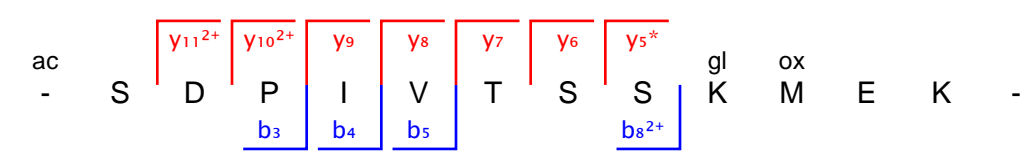
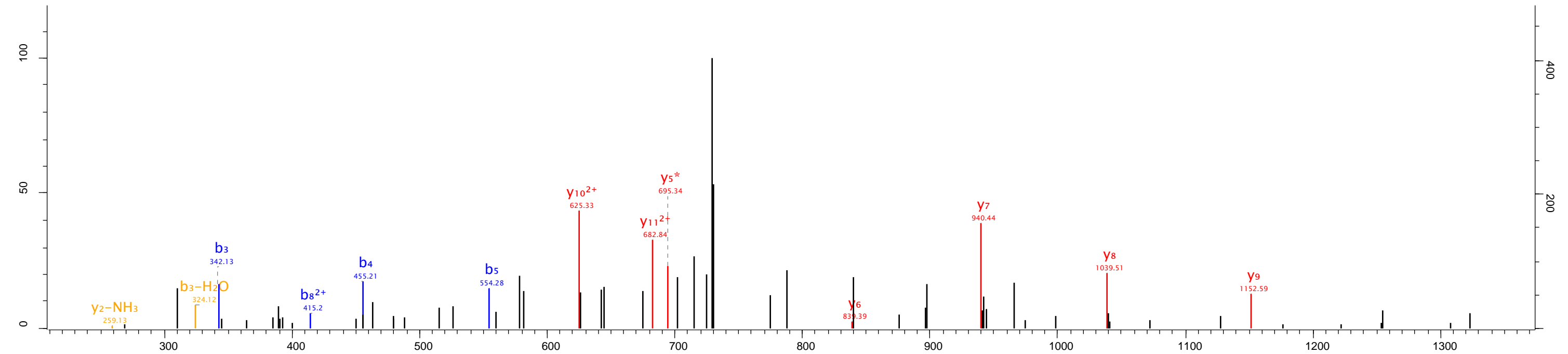
Raw file
tay_Yeast_Untreated_WCLip_GG_CID_01August14_04

Scan	Method	Score	m/z
44092	ITMS; CID	50.26	865.79



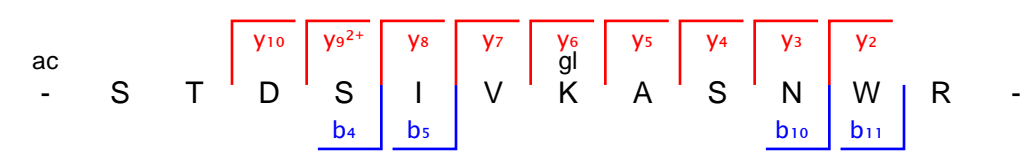
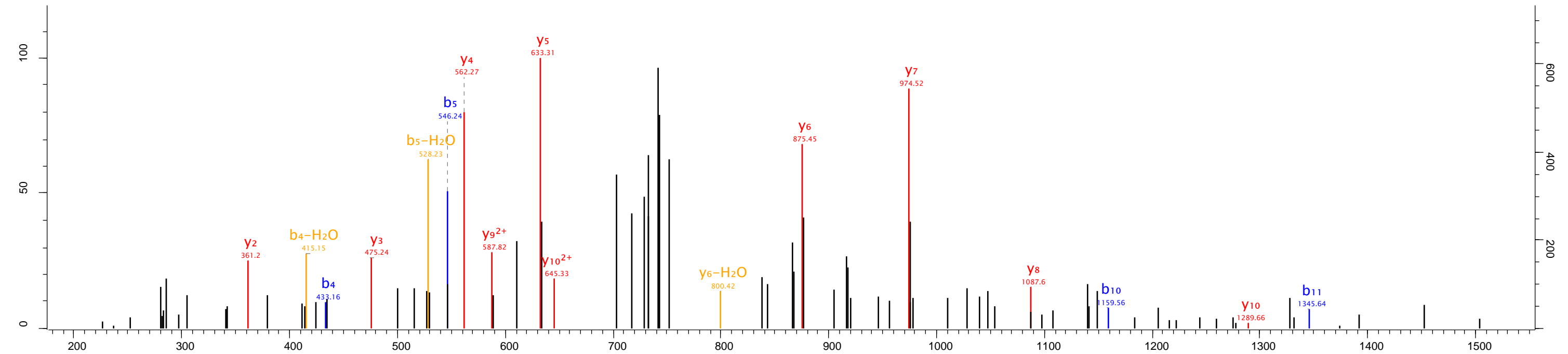


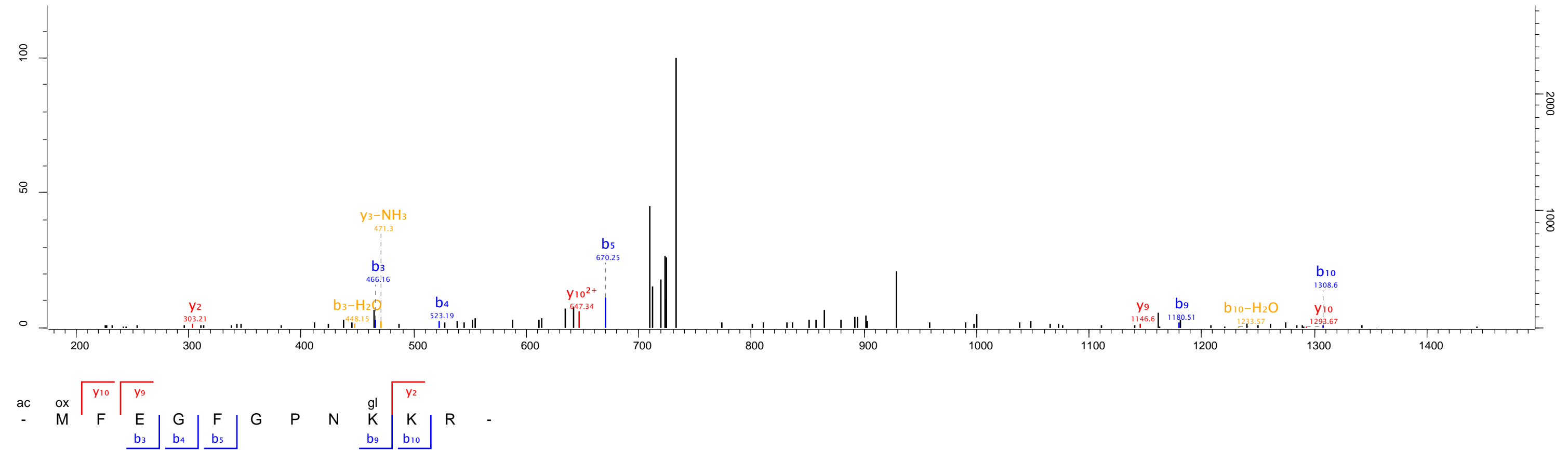


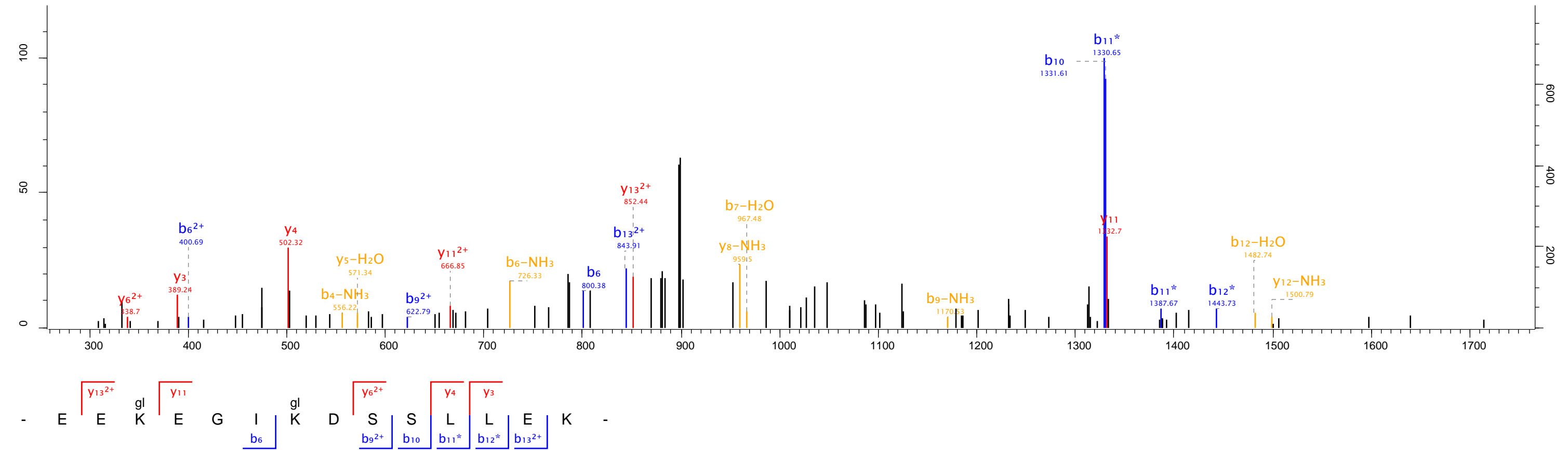


Raw file
tay_Yeast_Untreated_WCLip_GG_CID_A_06August14_03

Scan	Method	Score	m/z
18081	ITMS; CID	76.07	760.88







Raw file

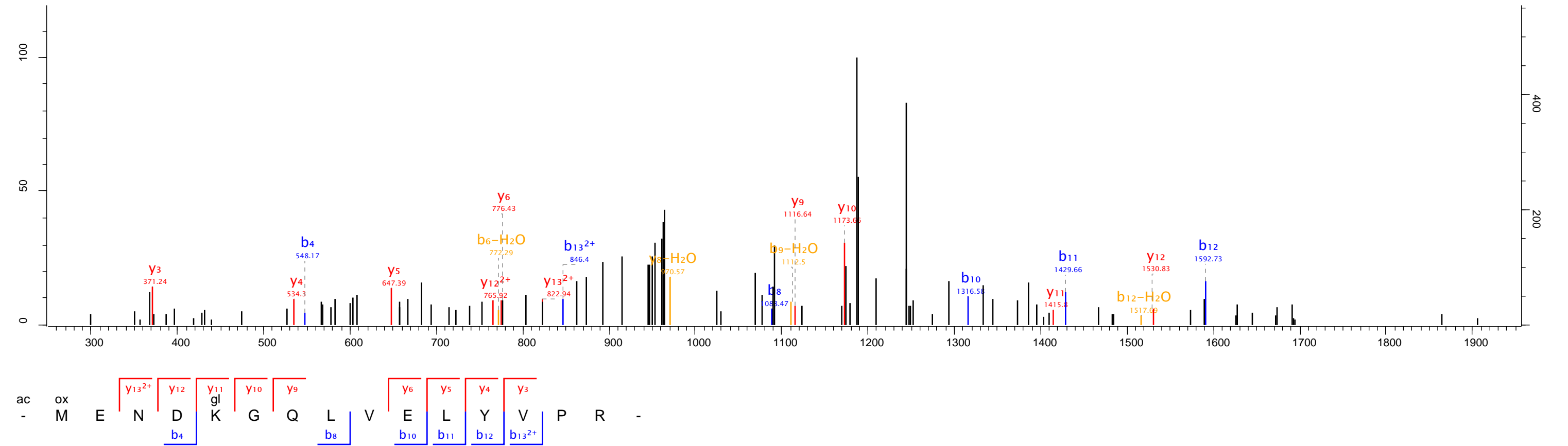
Scan26937

MethodITMS; CID

Score58.81

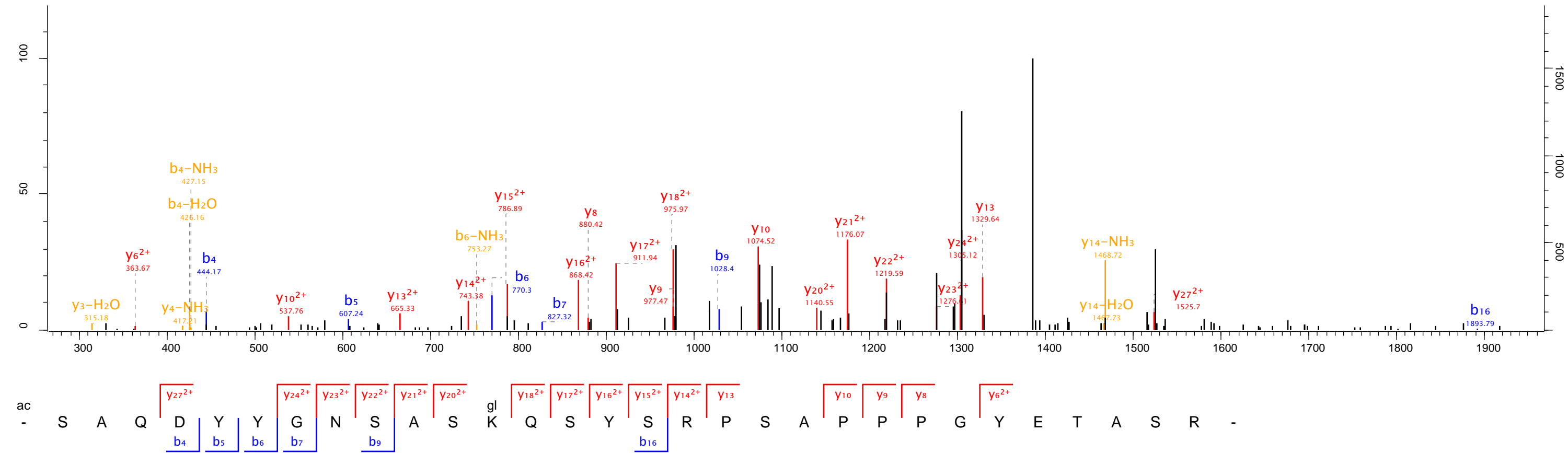
m/z981.98

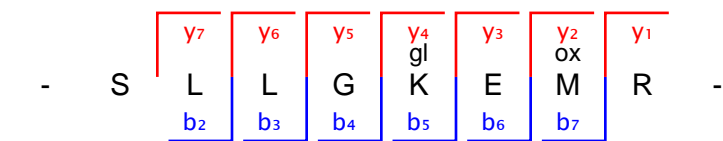
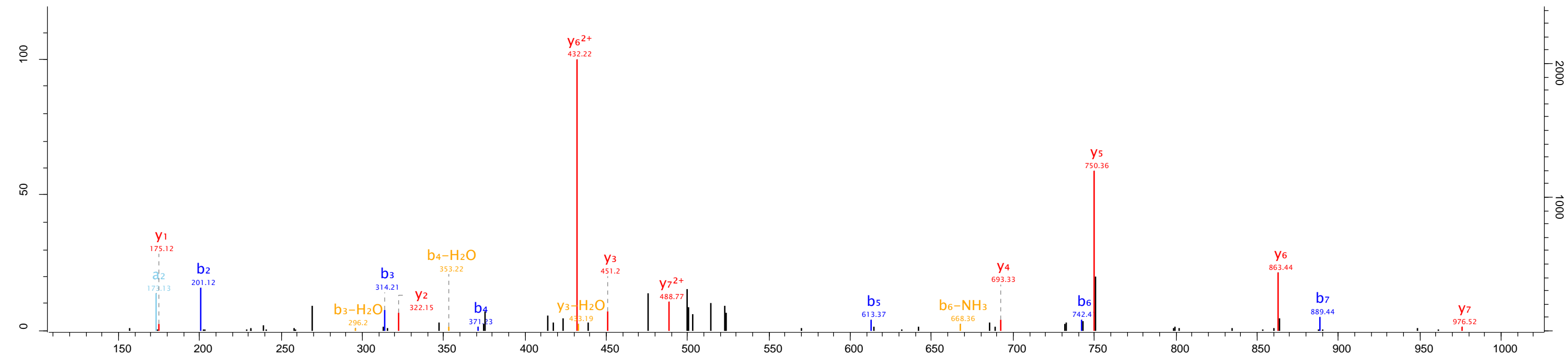
tay_Yeast_Untreated_WCLip_GG_CID_B_06August14_07



Raw file
tay_Yeast_Untreated_WCLip_GG_CID_C_06August14_11

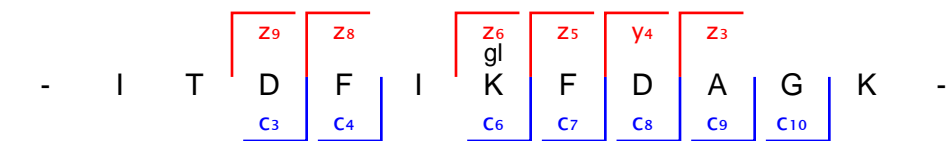
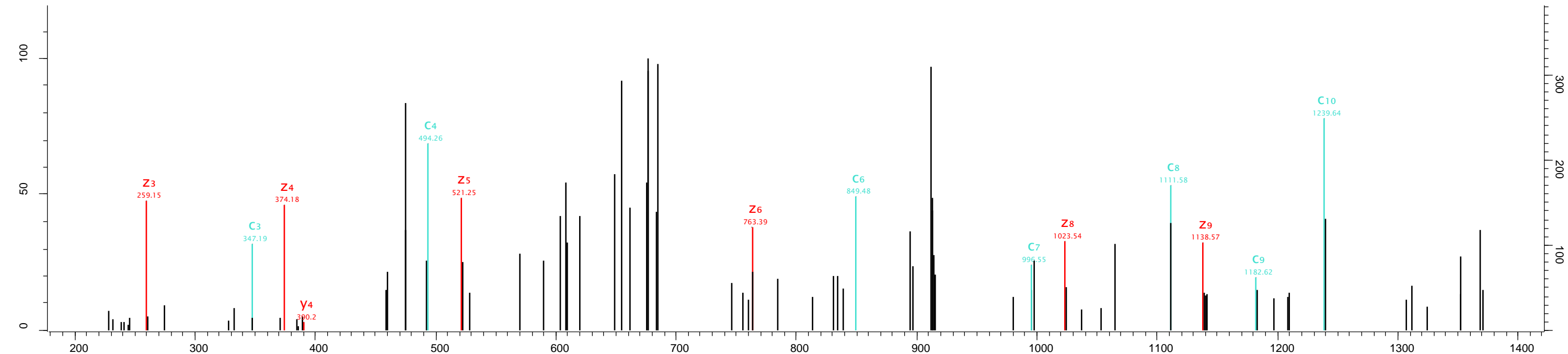
Scan	Method	Score	m/z
15497	ITMS; CID	81.97	1127.18

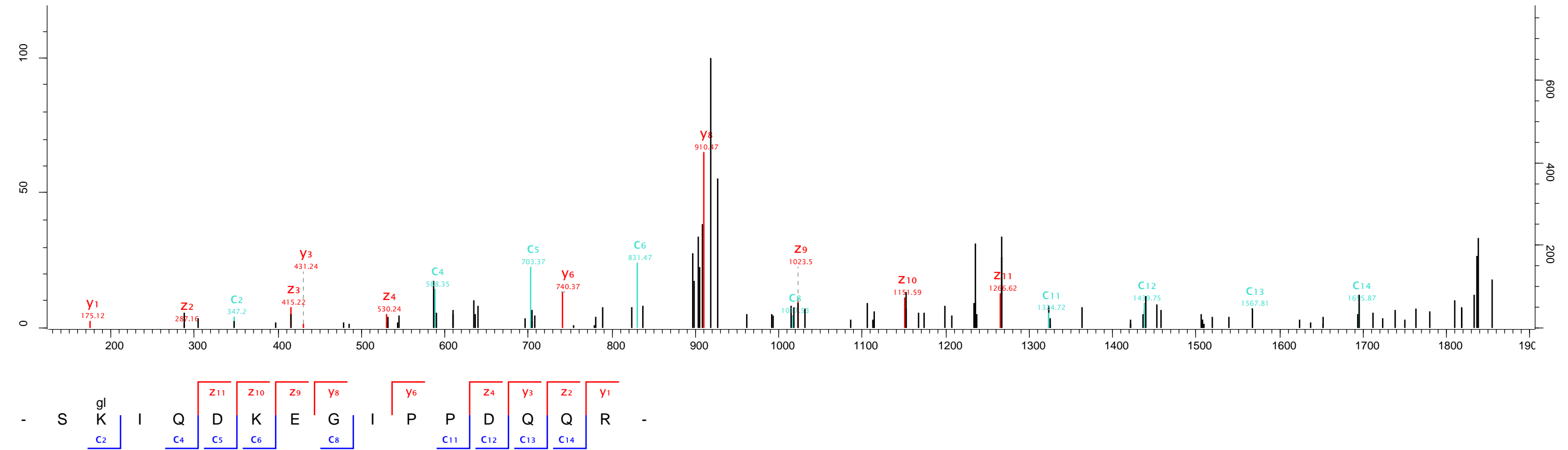




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

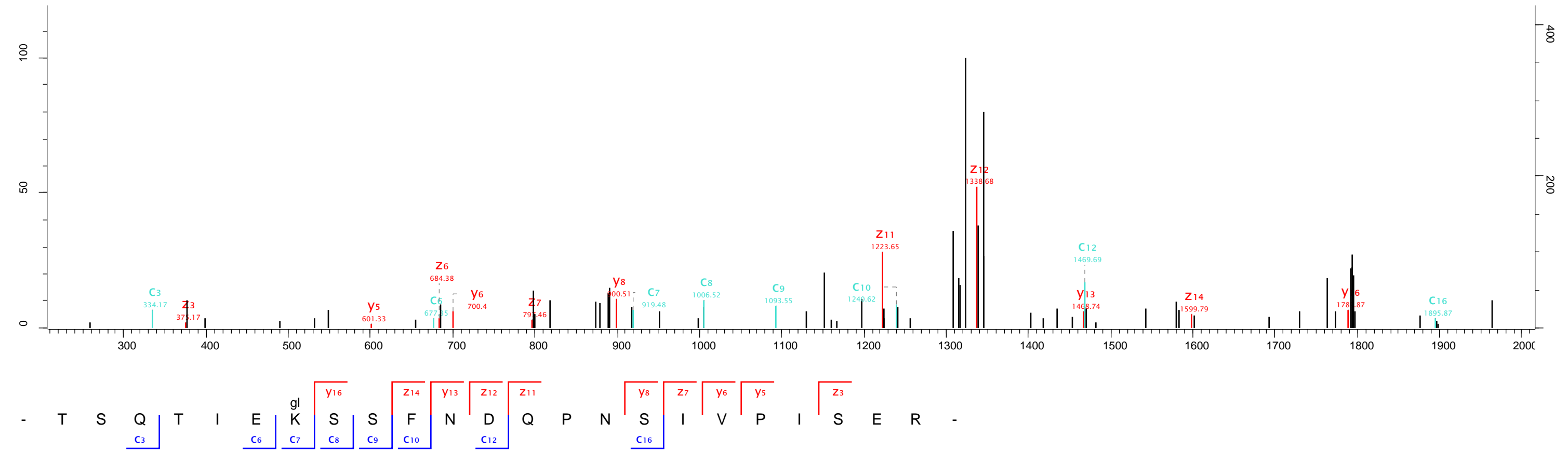
Scan	Method	Score	m/z
10022	ITMS; ETD	166.69	456.91

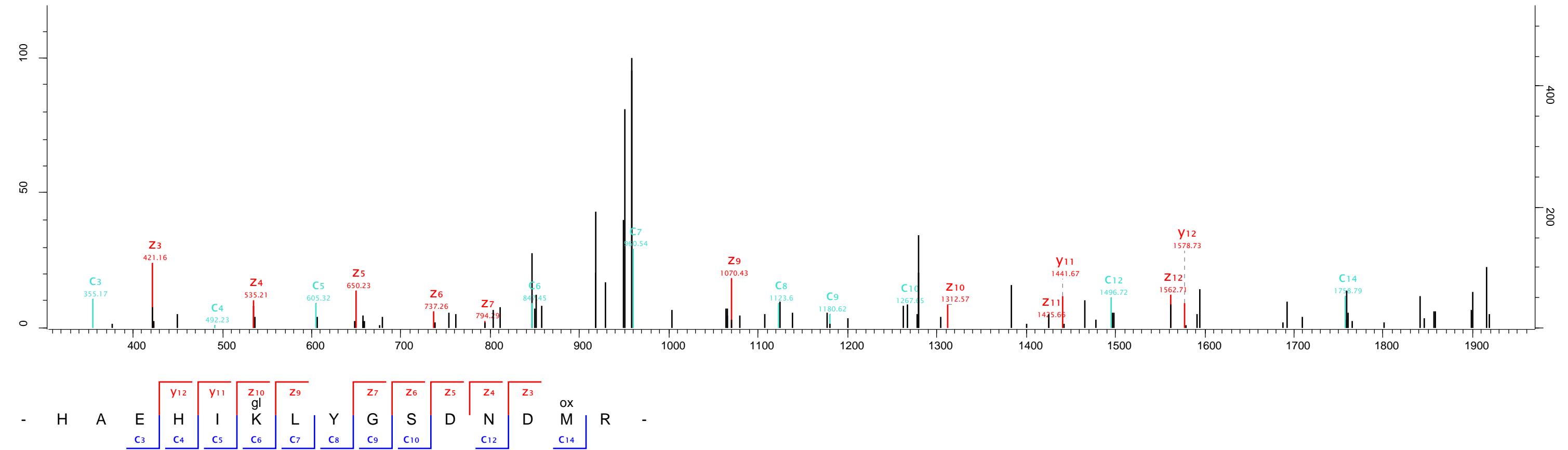




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

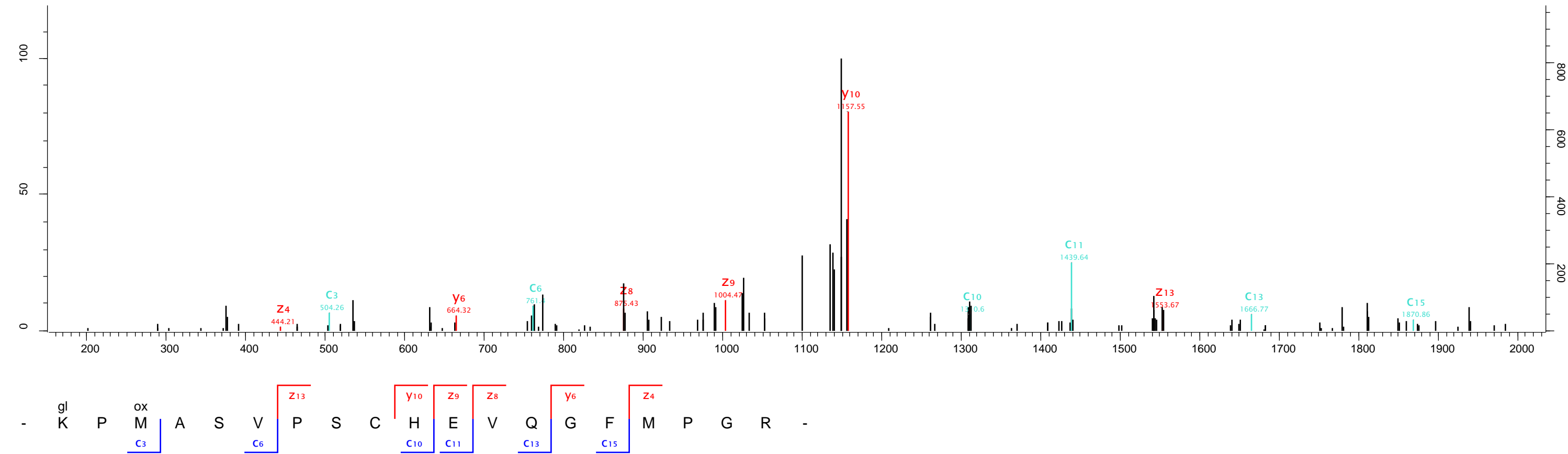
Scan	Method	Score	m/z
10318	ITMS; ETD	103.87	898.11

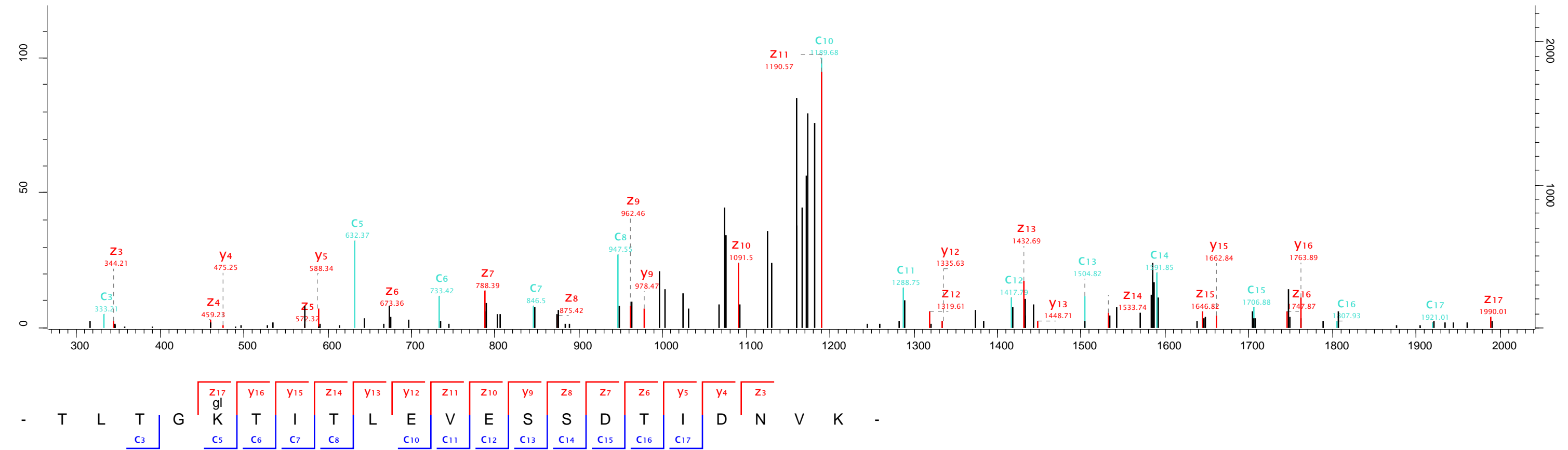


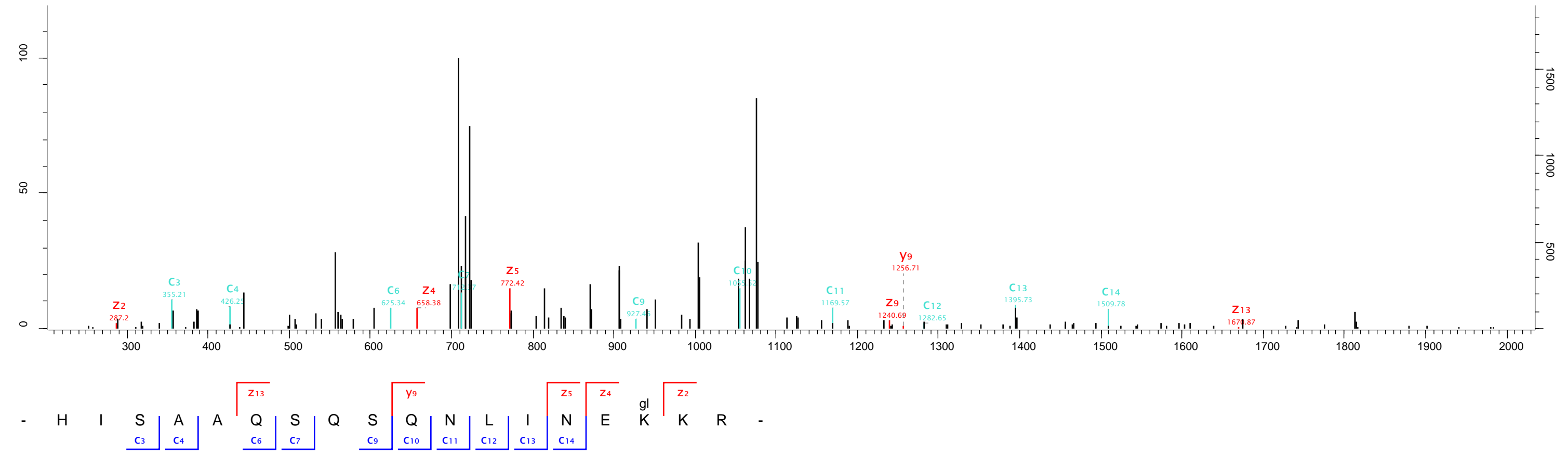


Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

Scan	Method	Score	m/z
1251	ITMS; ETD	58.56	771.69

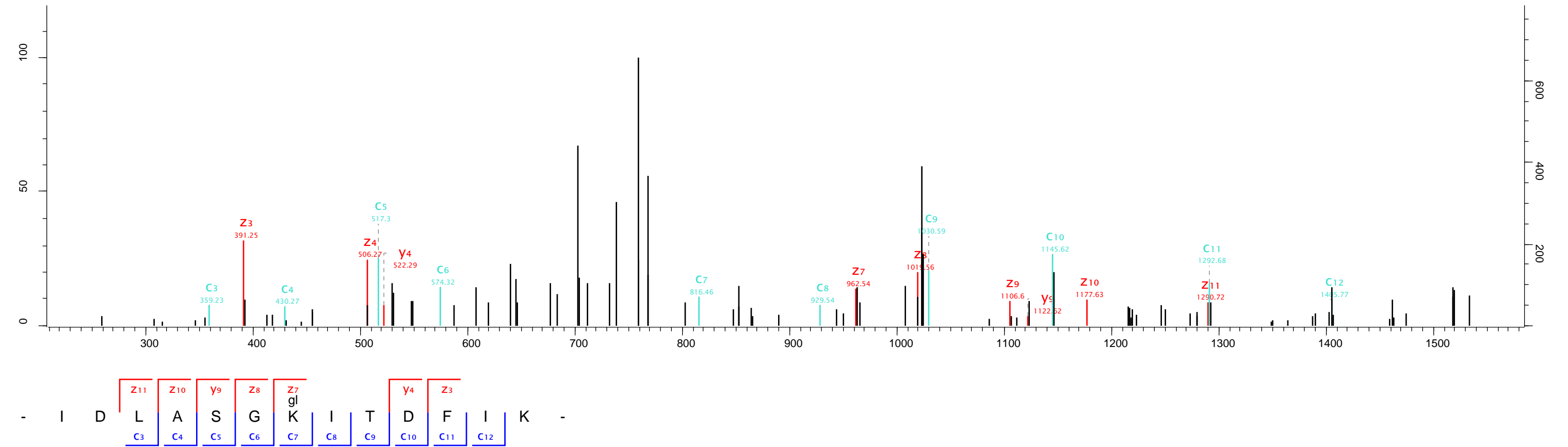


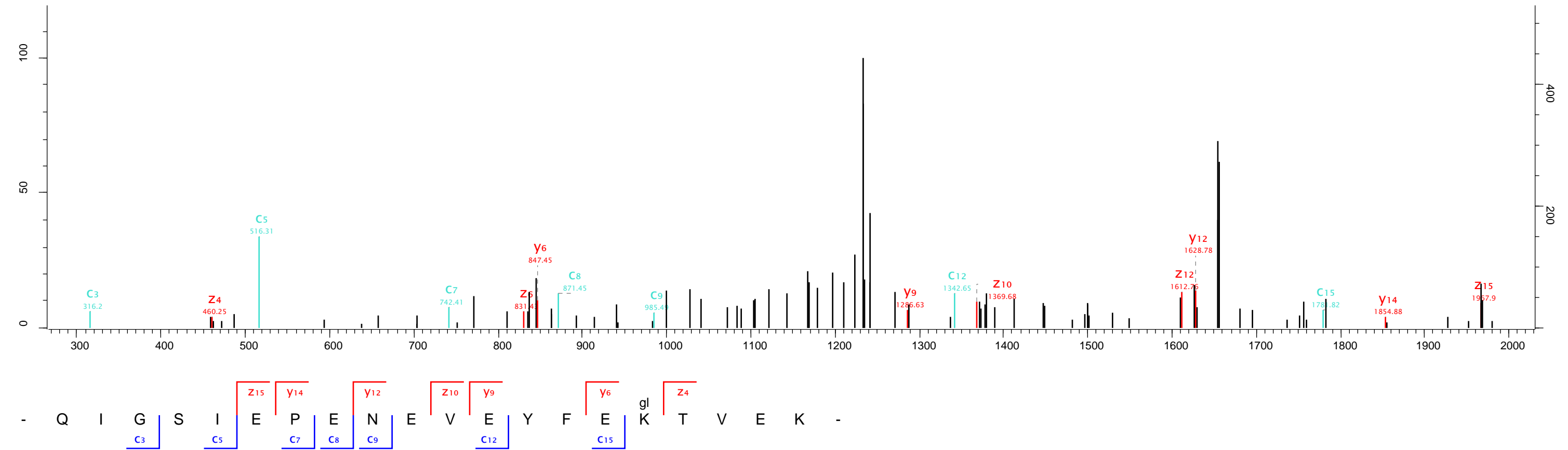




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

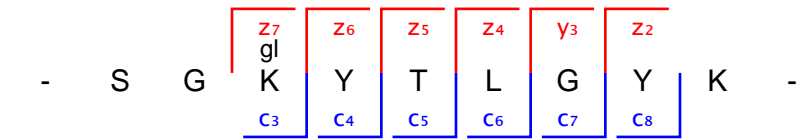
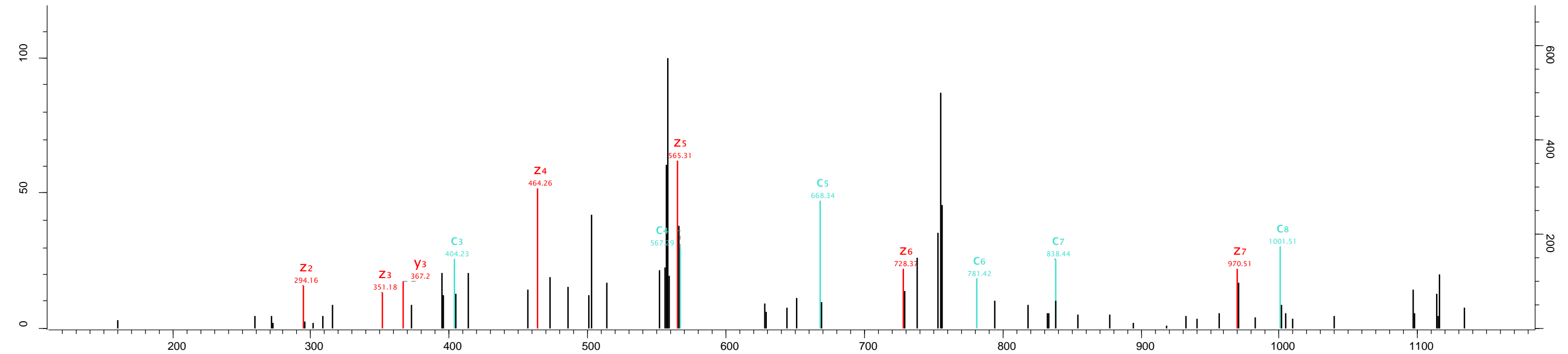
Scan	Method	Score	m/z
15245	ITMS; ETD	163.15	512.29





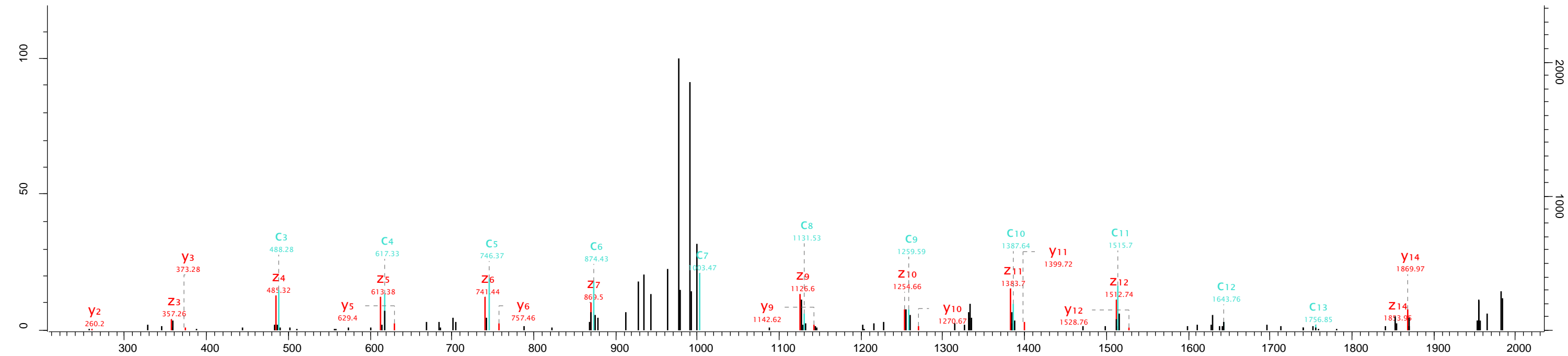
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

Scan	Method	Score	m/z
1840	ITMS; ETD	128.48	377.53



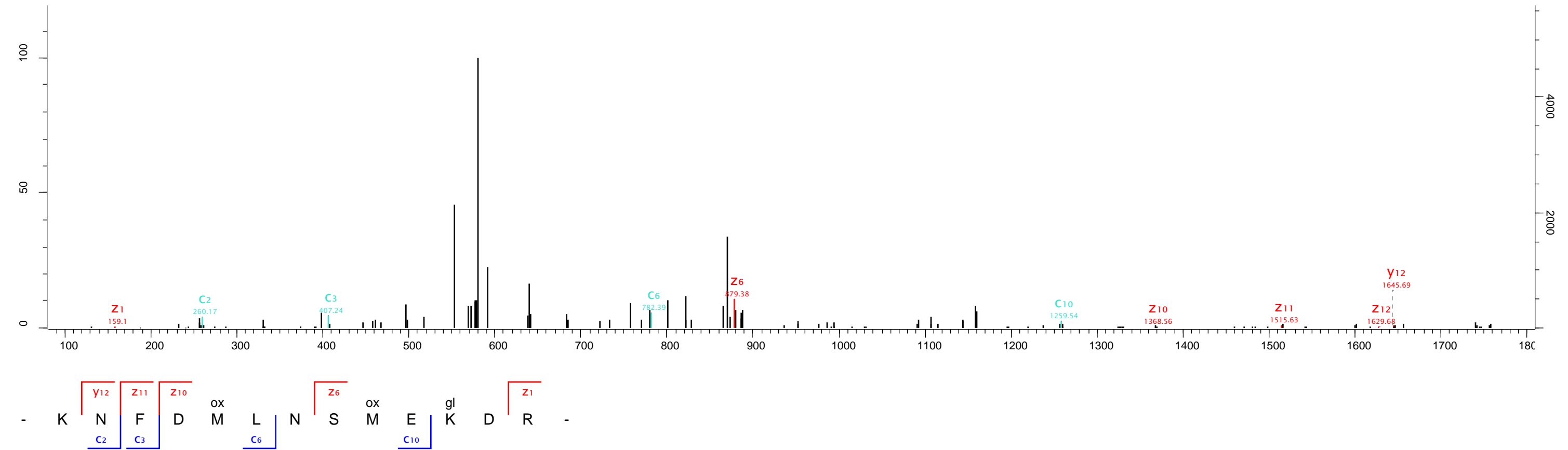
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

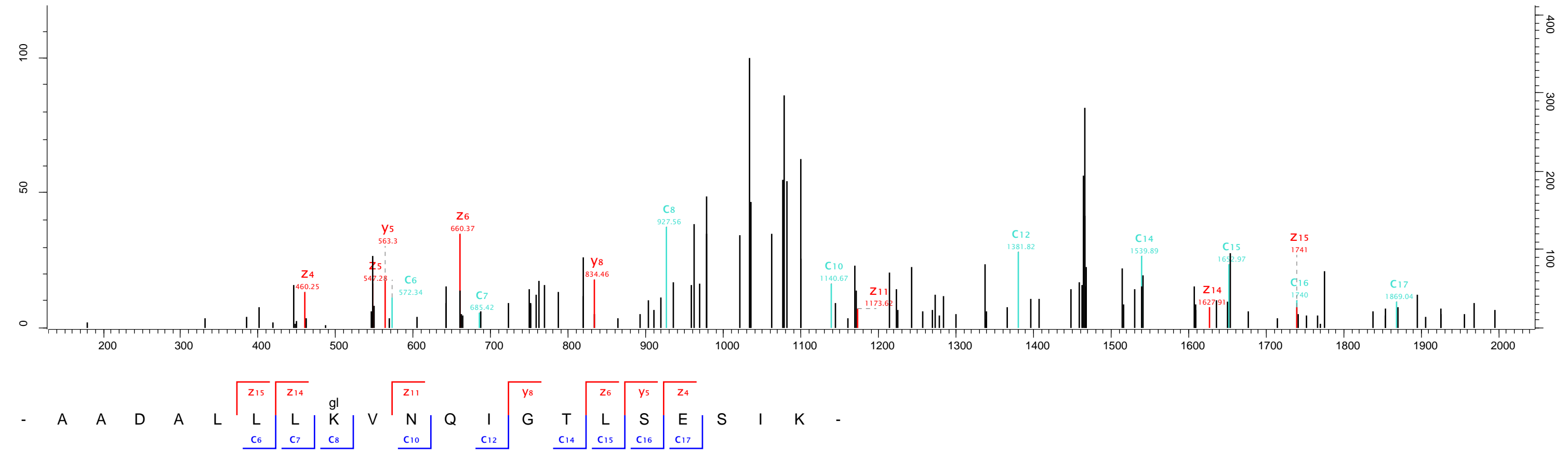
Scan	Method	Score	m/z
1888	ITMS; ETD	339.48	667.01

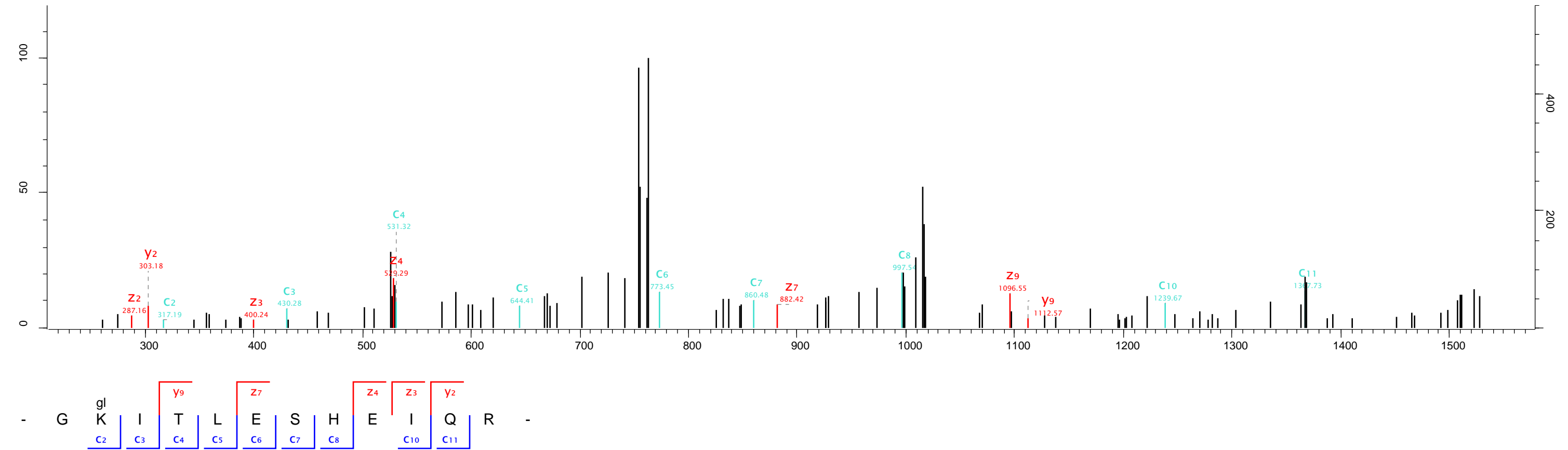


- E -
- E K V E E Q E Q Q Q Q Q I I K -
C3 C4 C5 C6 C7 C8 C9 C10 C11 C12 C13

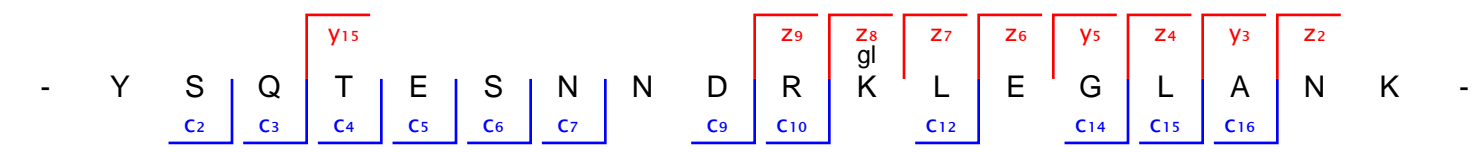
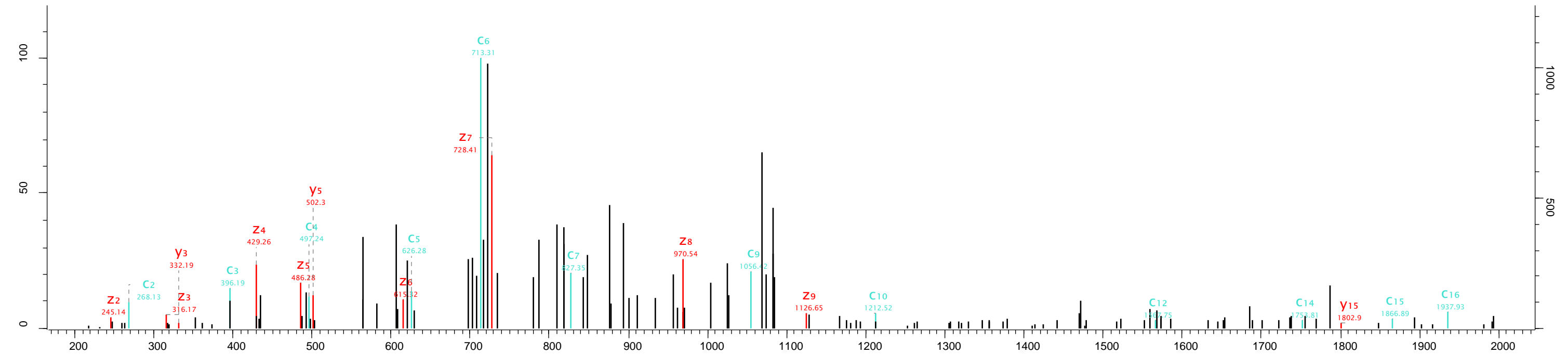
Peptide sequence: E K V E E Q E Q Q Q Q Q I I K. The sequence is annotated with fragmentation sites: y14 (K), y12 (E), y11 (E), y10 (Q), y9 (E), y7 (Q), y6 (Q), y5 (Q), y4 (Q), y3 (I), y2 (I). The corresponding b-ion fragments are labeled C3 through C13.

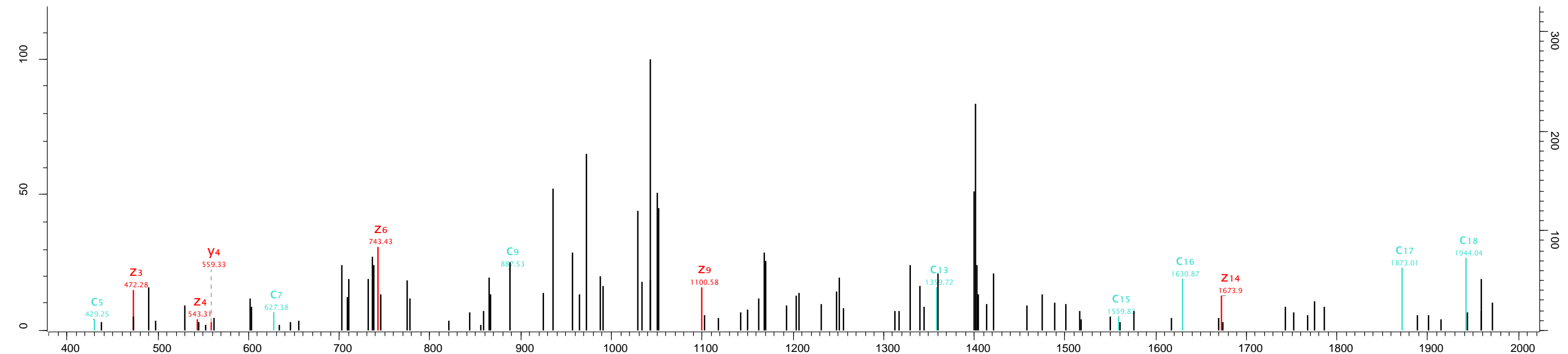






tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

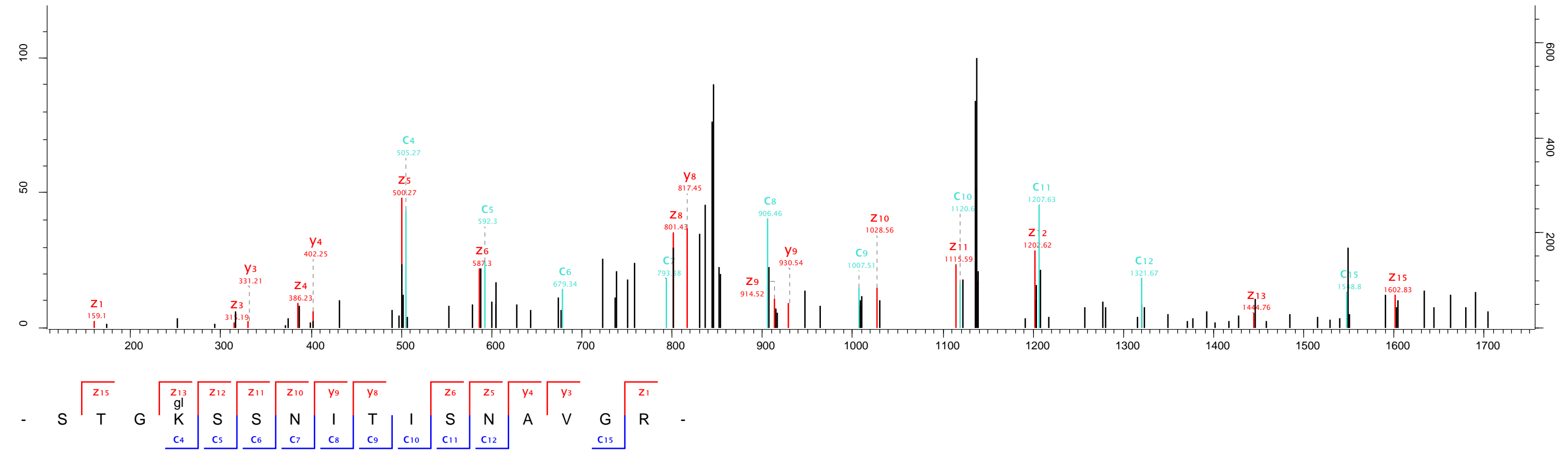


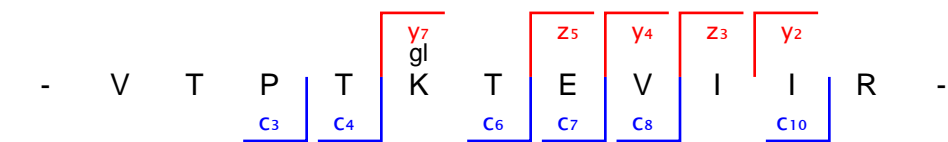
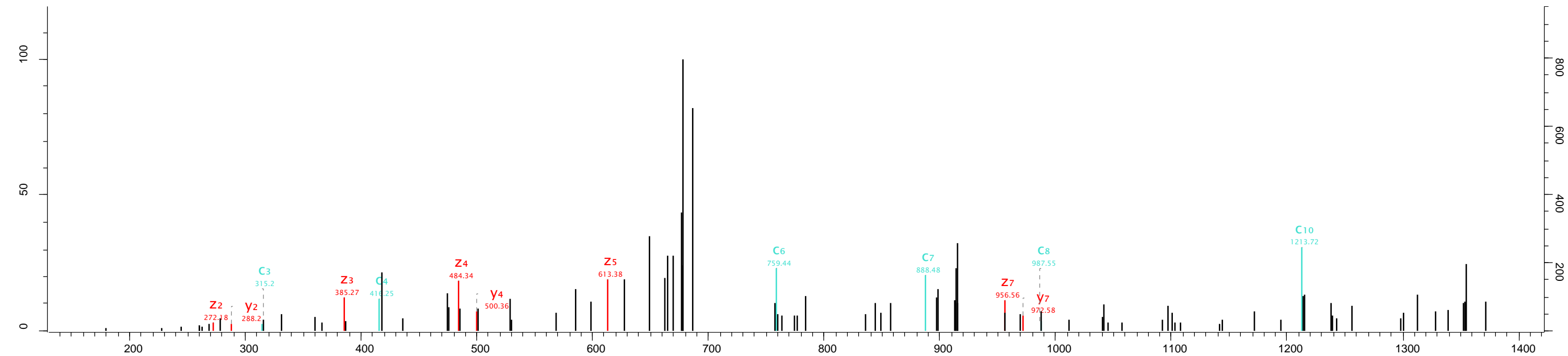


- A A A P T V V F L D E L D S I A K A R -

Labels below the sequence: C5 (under T), C7 (under V), C9 (under L), C13 (under D), C15 (under I), C16 (under A), C17 (under K), C18 (under A).

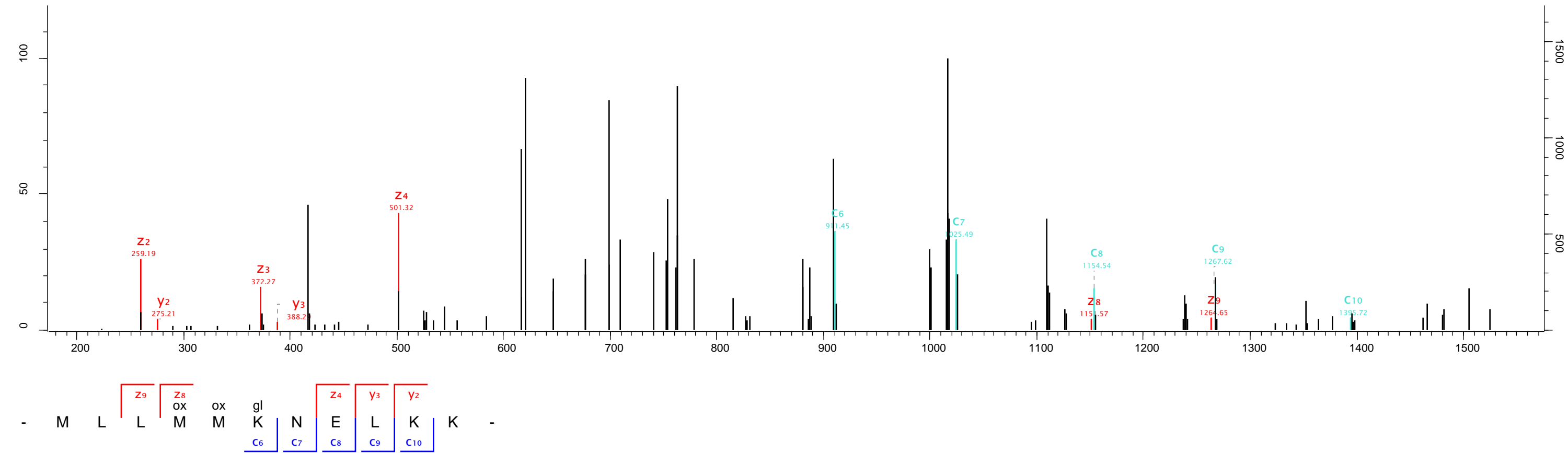
Labels above the sequence: Z14 (above V), Z9 (above E), Z6 (above S), Y4 (above A), Z3 (above K).





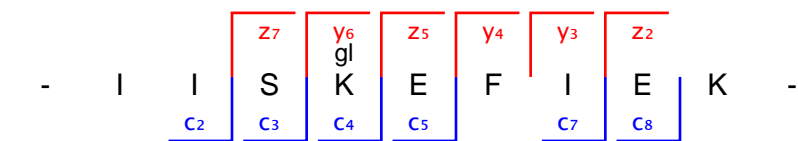
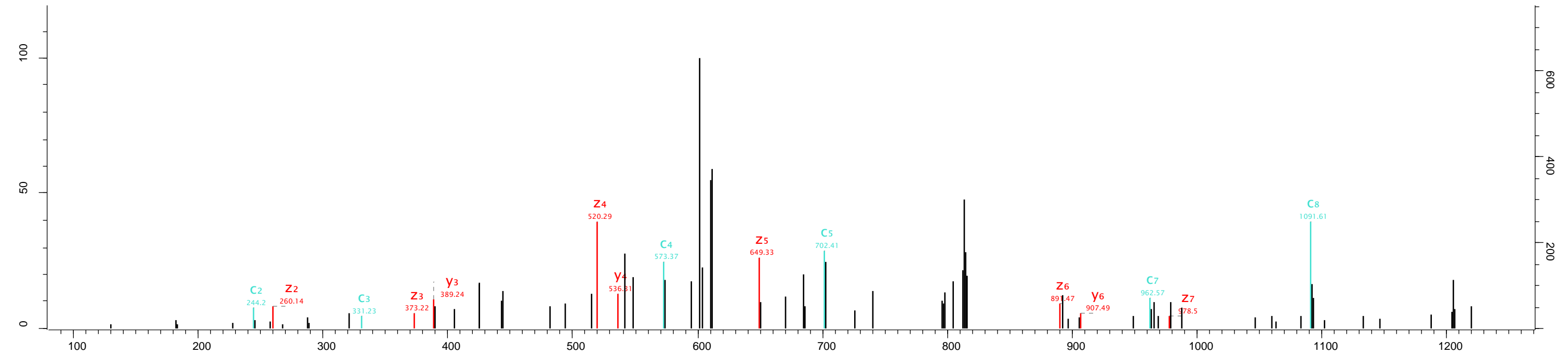
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

Scan	Method	Score	m/z
3847	ITMS; ETD	111.5	508.94



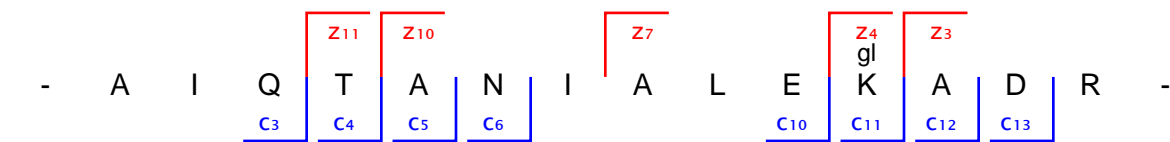
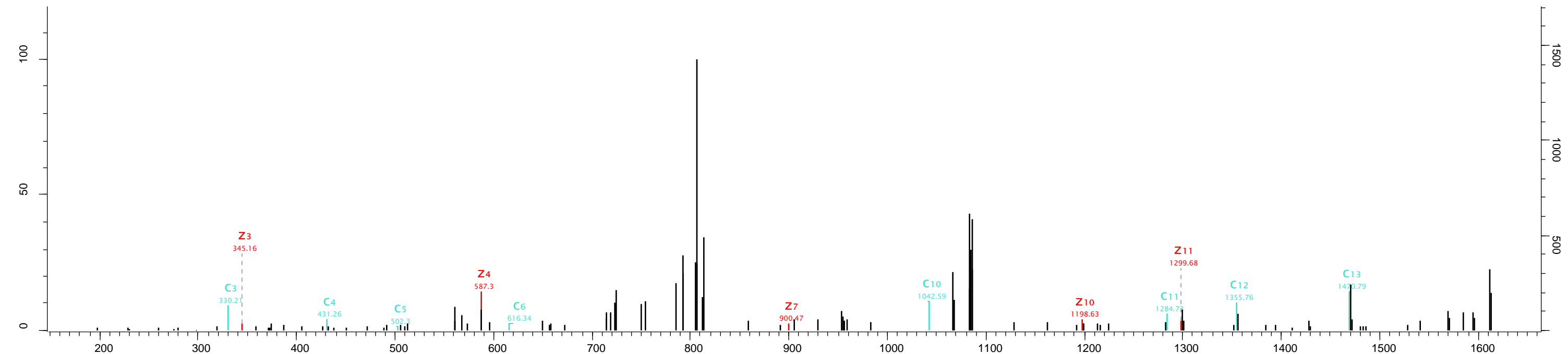
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

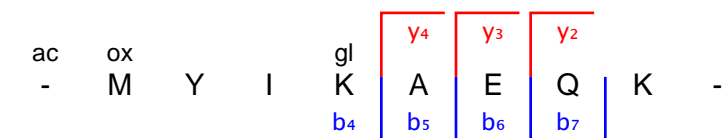
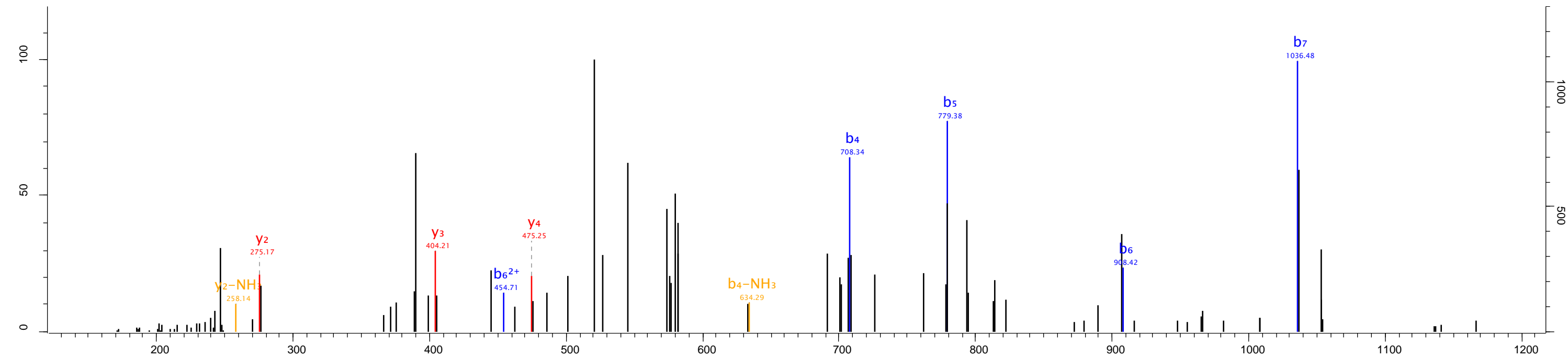
Scan	Method	Score	m/z
4538	ITMS; ETD	107.11	407.57

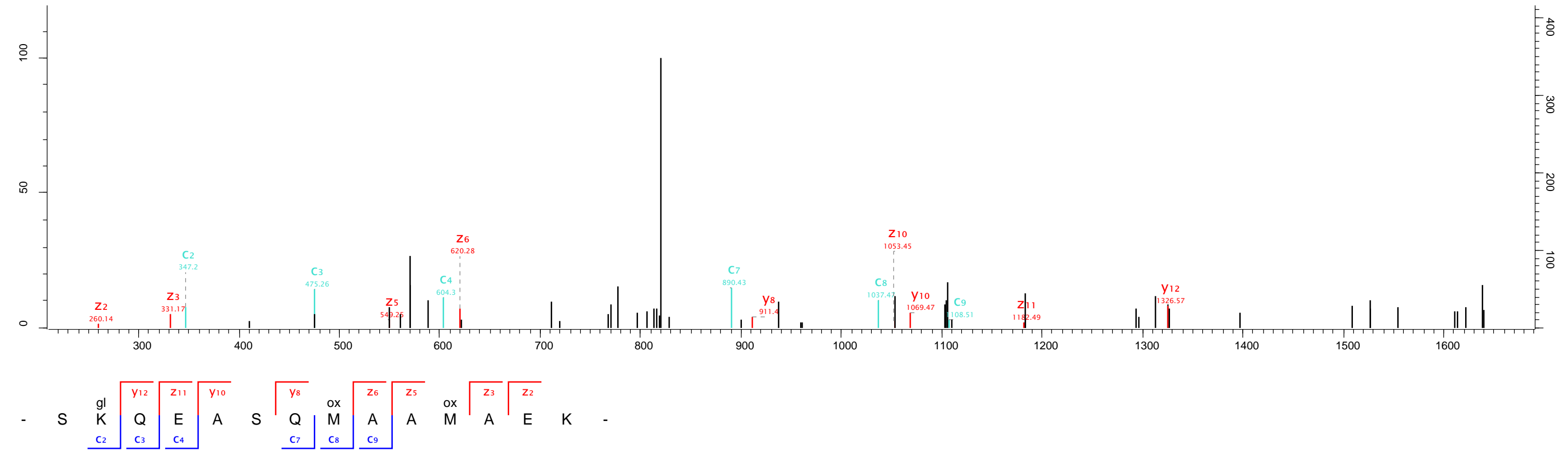


tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

Scan	Method	Score	m/z
5600	ITMS; ETD	96.67	543.3

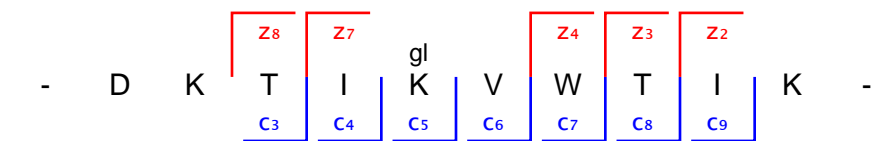
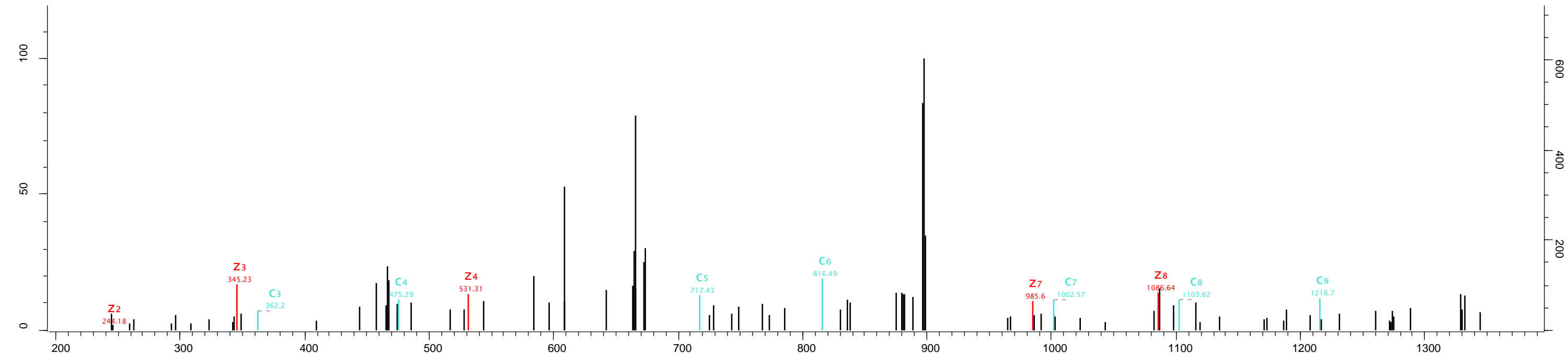


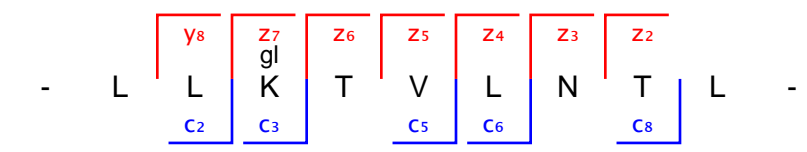
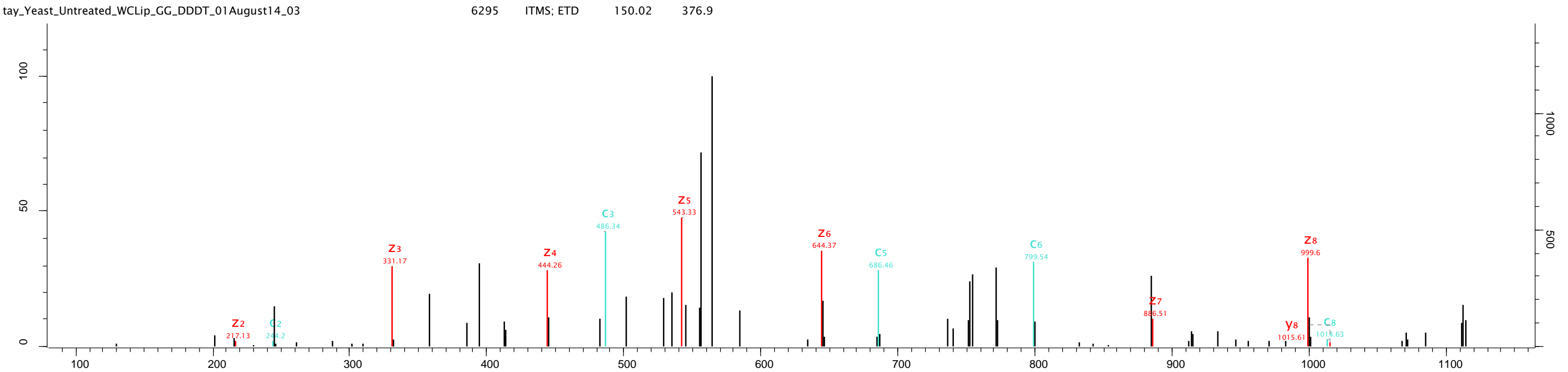




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

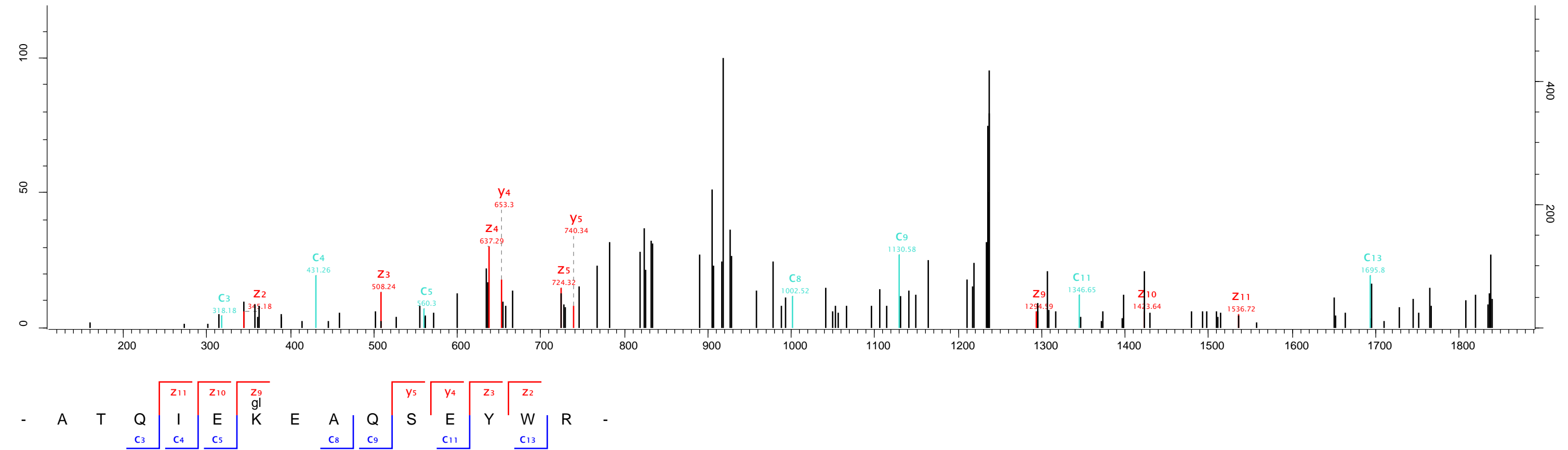
Scan	Method	Score	m/z
6243	ITMS; ETD	99	449.27

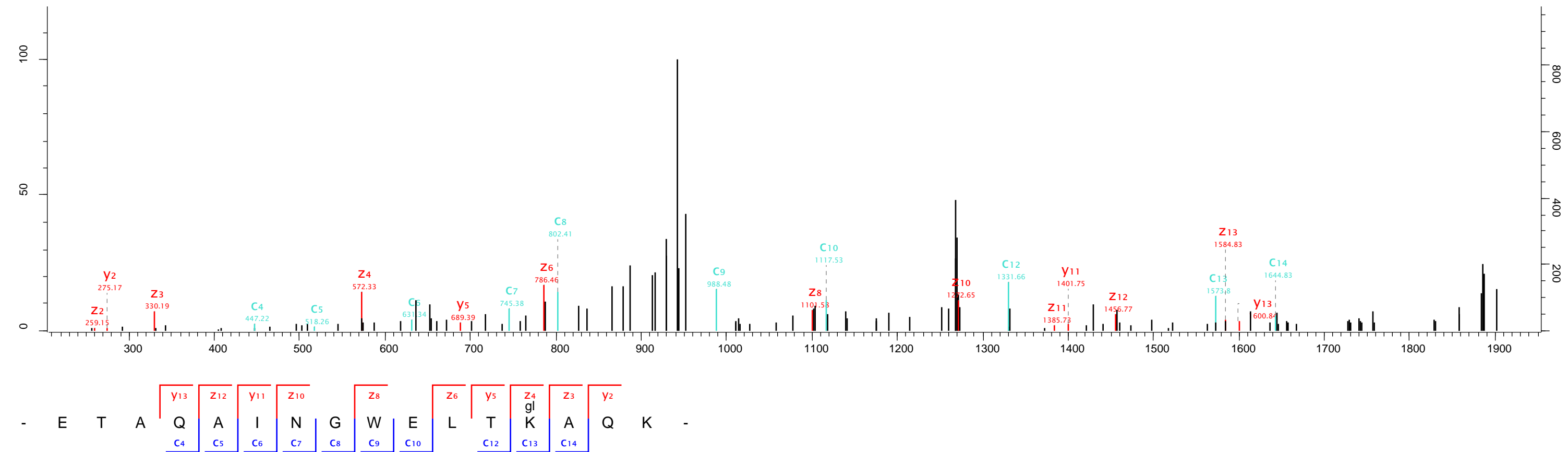




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

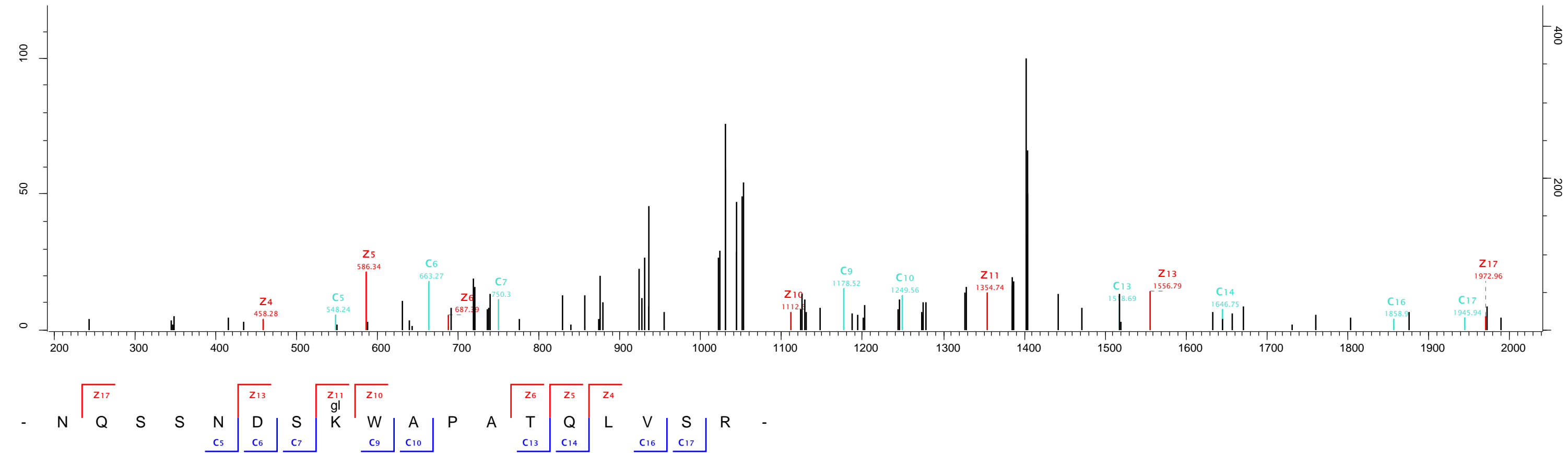
Scan	Method	Score	m/z
6825	ITMS; ETD	117.53	618.63





Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03

Scan	Method	Score	m/z
8113	ITMS; ETD	84.61	702.01

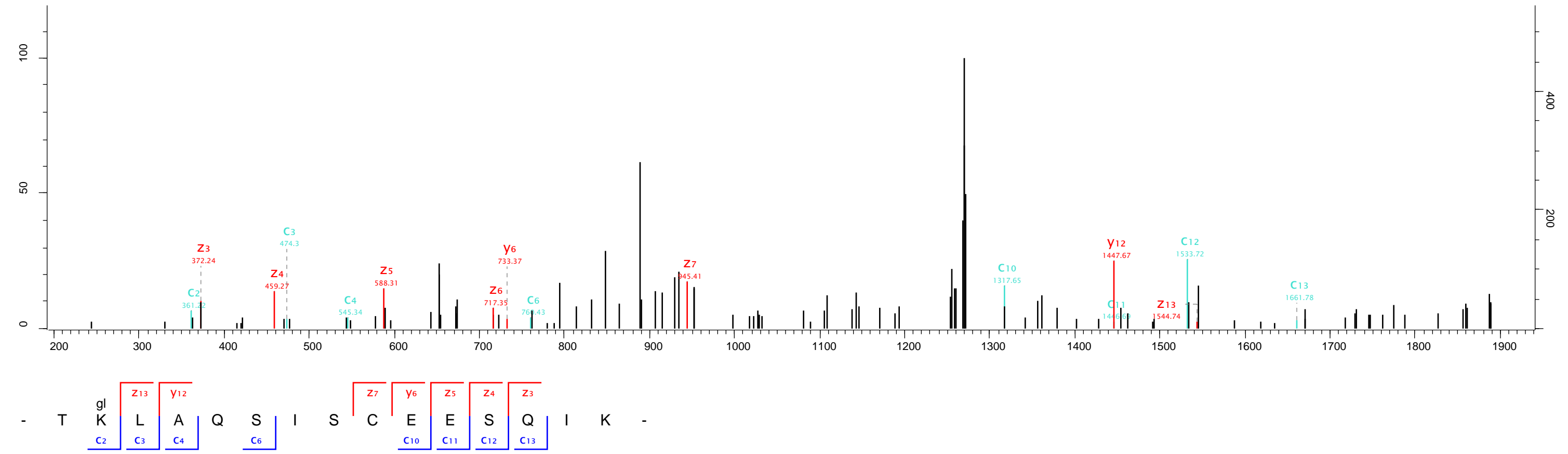


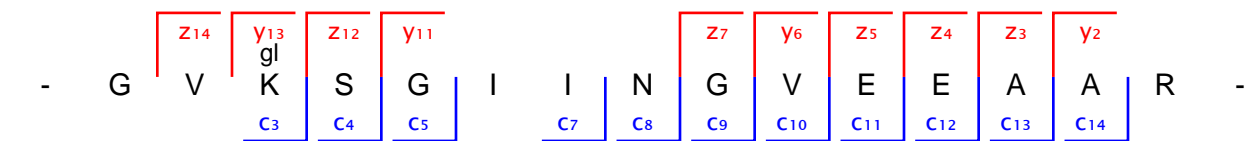
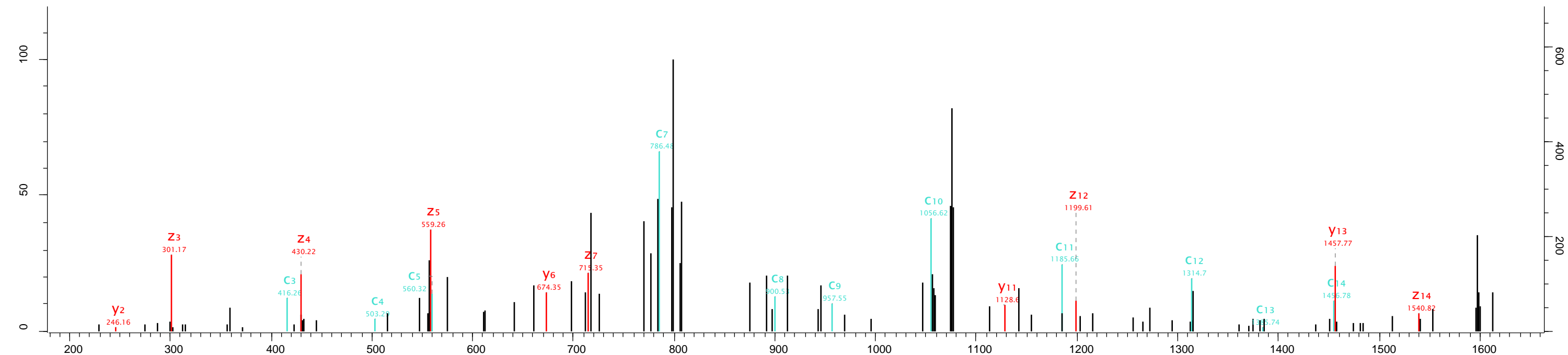
Raw file

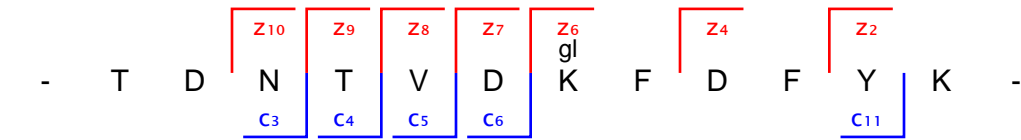
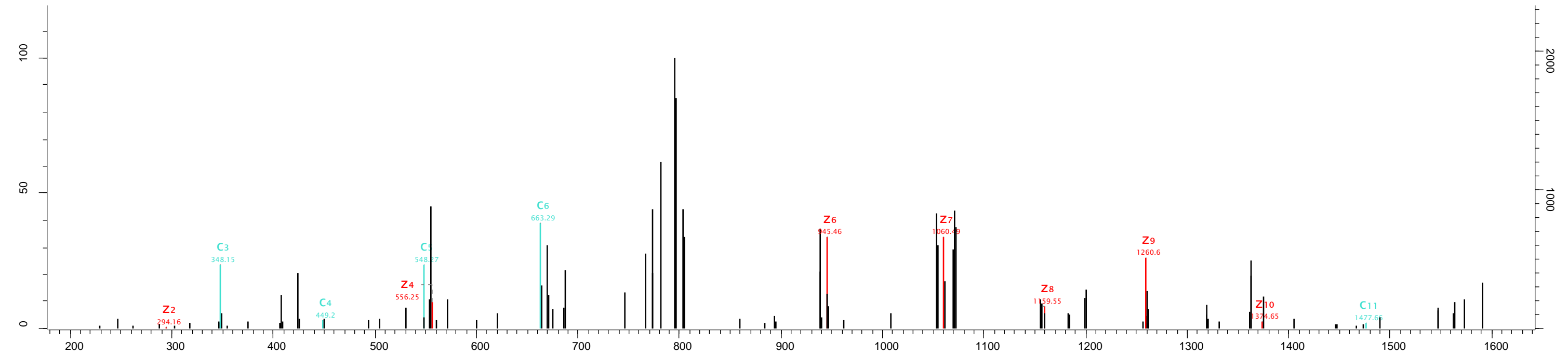
ScanMethodScorem/z

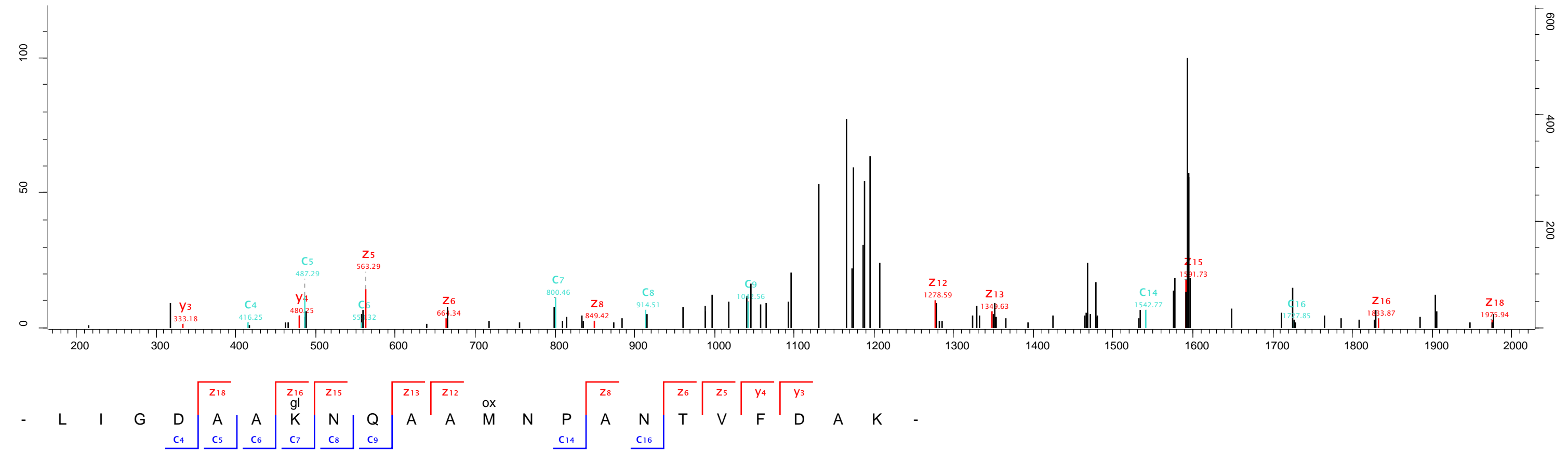
8496ITMS; ETD109.99635.65

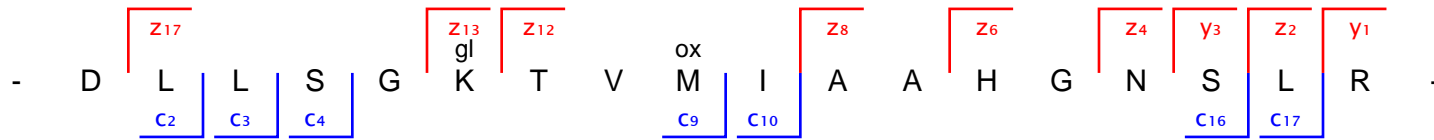
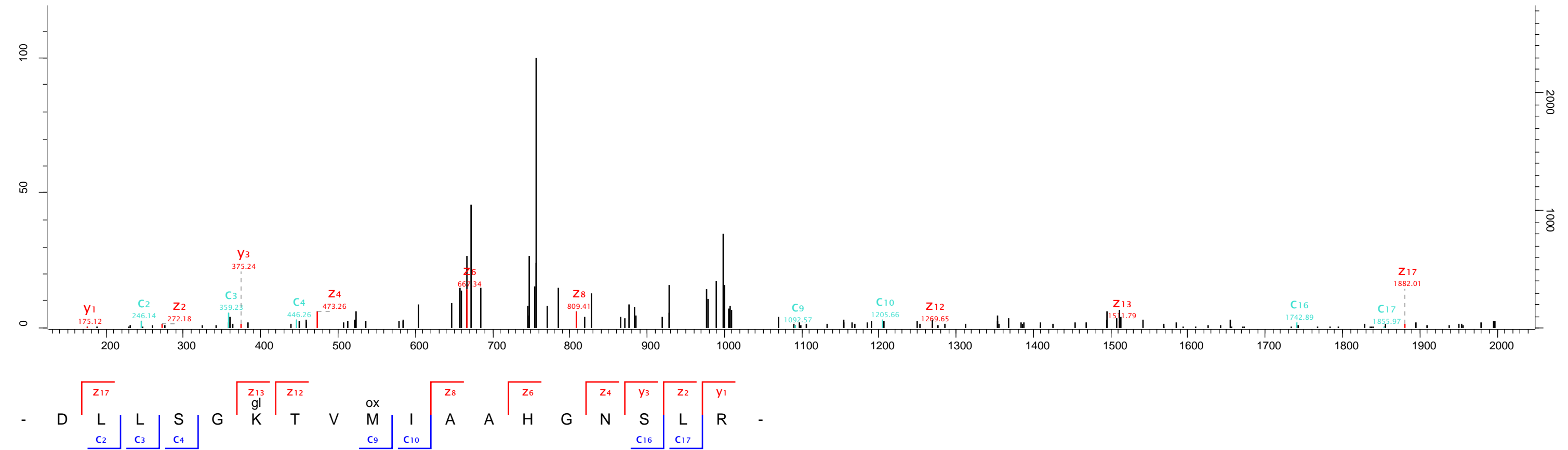
tay_Yeast_Untreated_WCLip_GG_DDDT_01August14_03



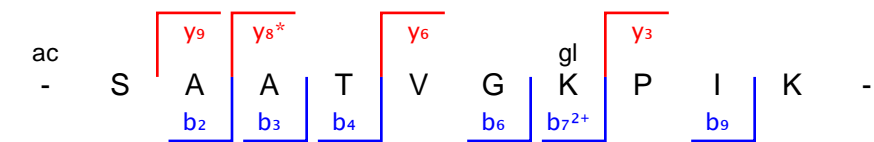
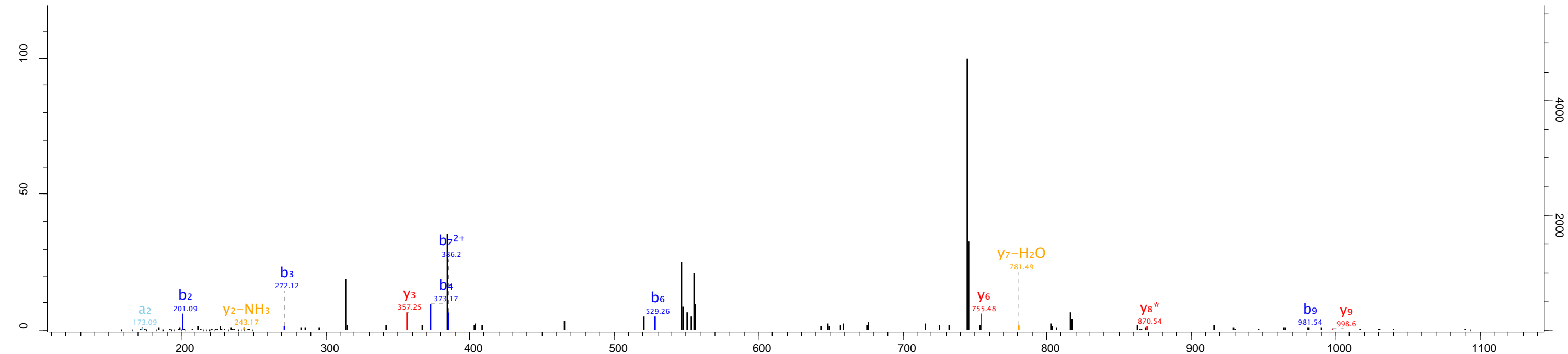






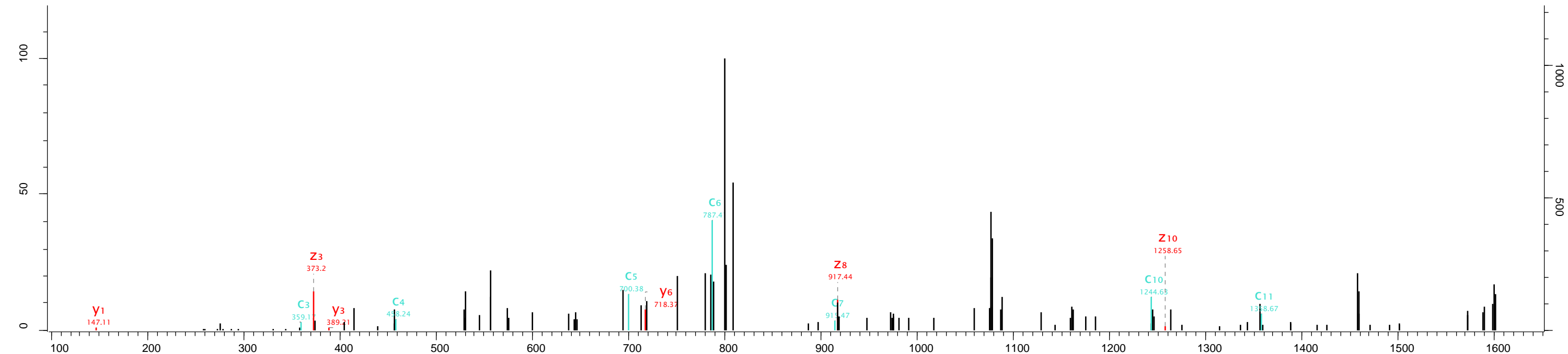


Raw file	Scan	Method	Score	m/z
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03	10568	ITMS; CID	52.73	565.3



Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

Scan	Method	Score	m/z
11574	ITMS; ETD	75.59	539.3

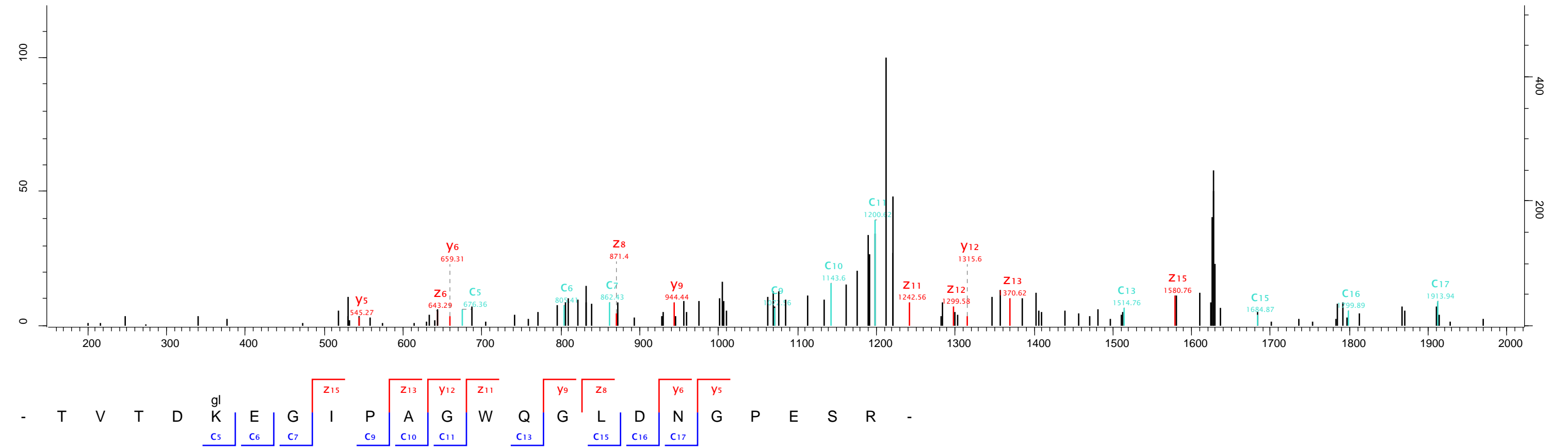


ac
- M A P V K S Q E S I N Q K -

Fragmentation sites (C3-C11) and charge state (Z10, Z8, Y6, Y3, Y1) are indicated by brackets and labels above the sequence.

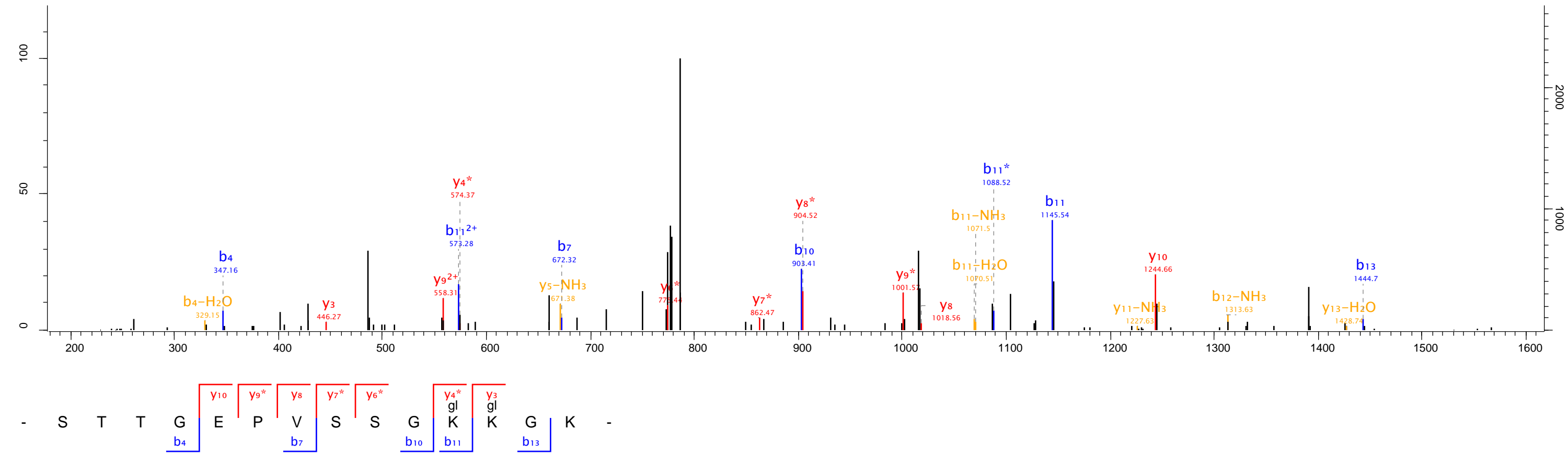
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

Scan	Method	Score	m/z
14025	ITMS; ETD	107.09	814.73



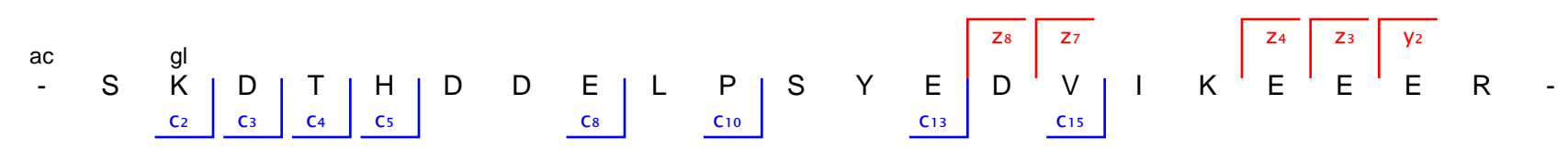
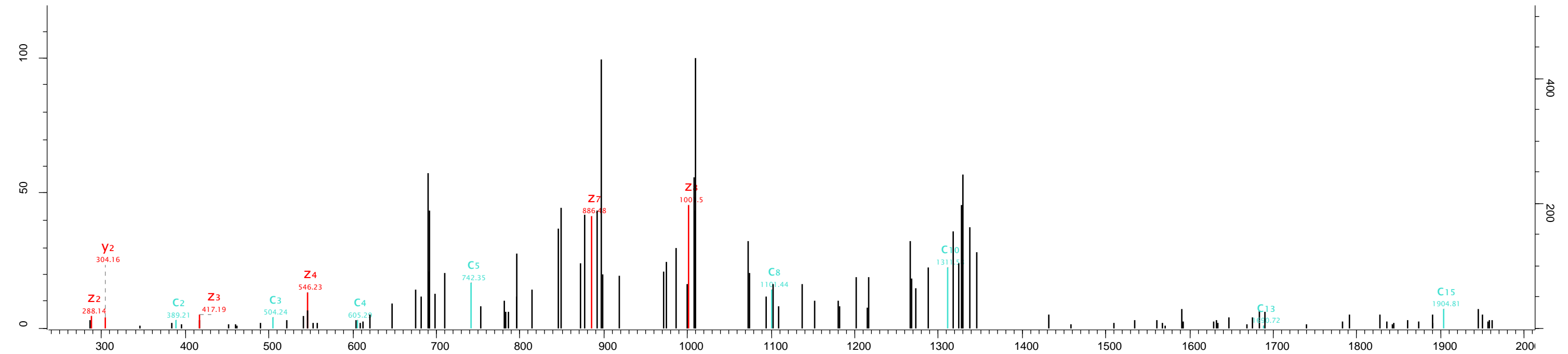
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

Scan	Method	Score	m/z
14363	ITMS; CID	77.05	795.9



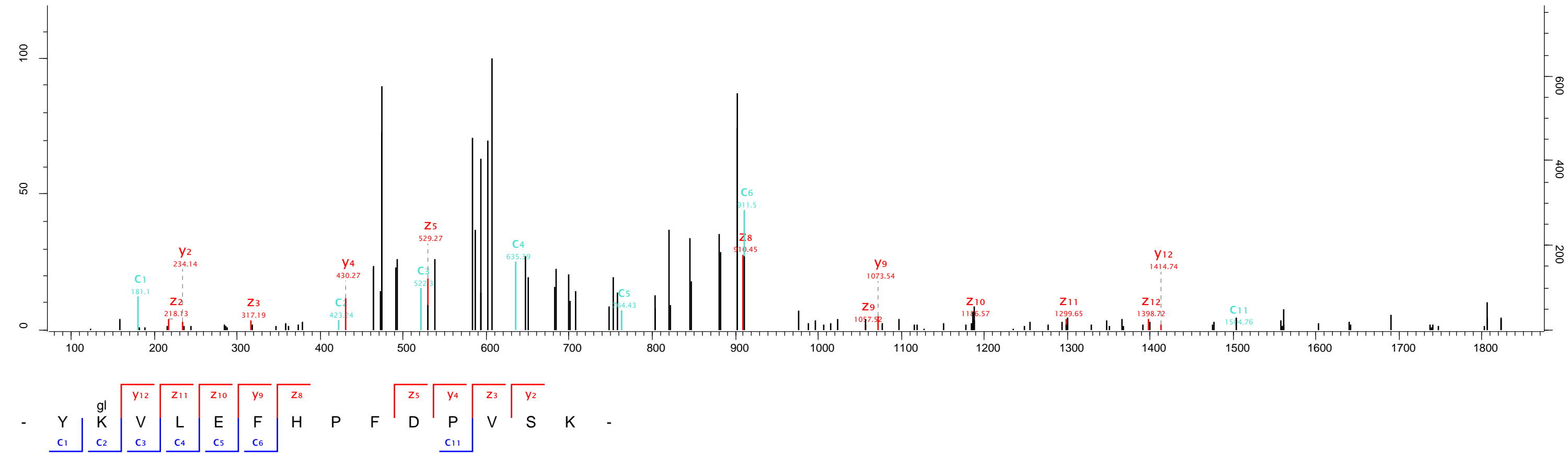
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

Scan	Method	Score	m/z
14758	ITMS; ETD	64.8	673.56



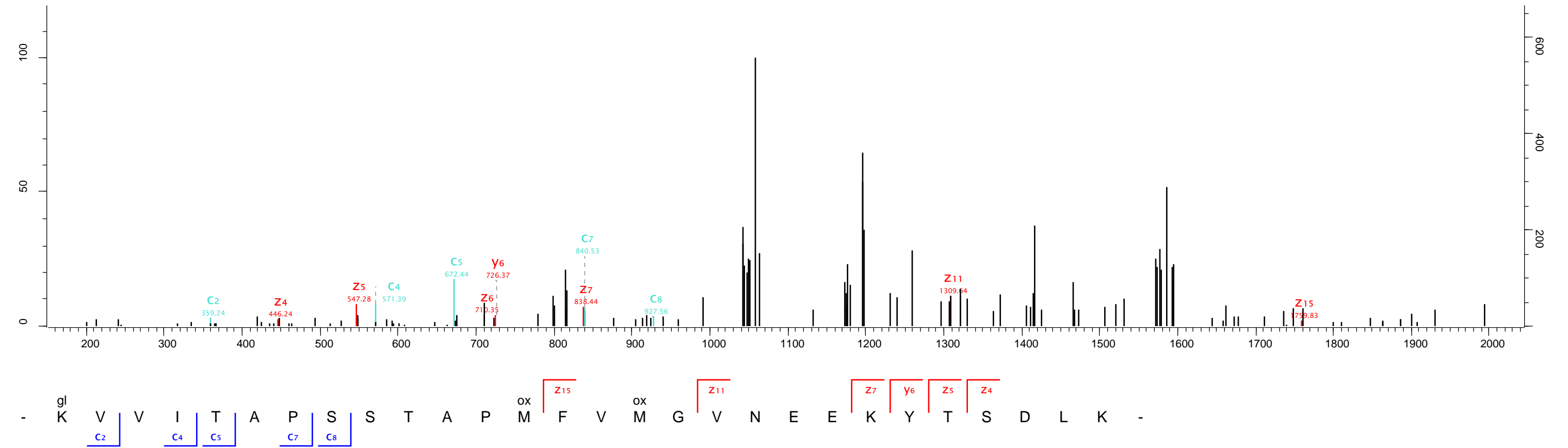
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

Scan	Method	Score	m/z
16399	ITMS; ETD	128.88	455.99

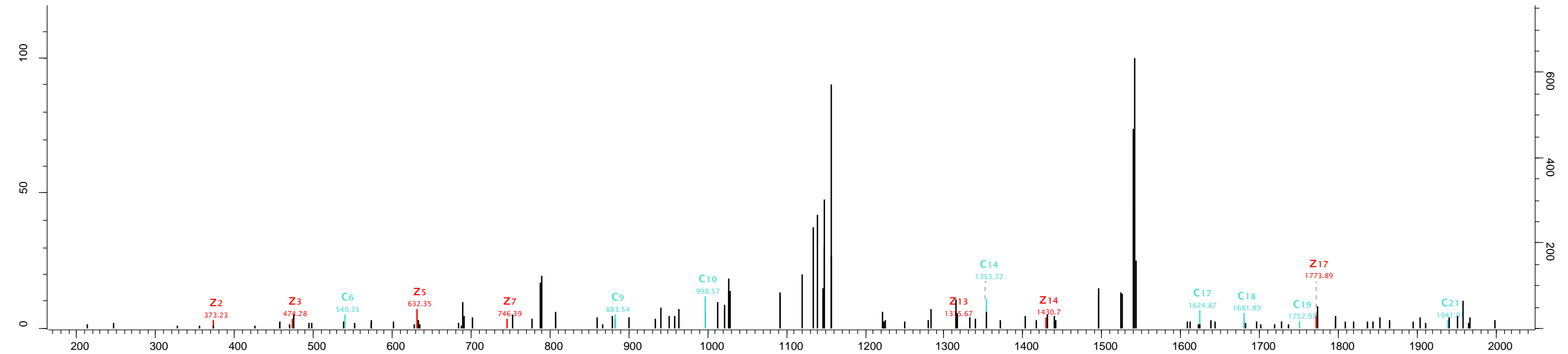


Raw file
tay_Yeast_Untreated_WCLip_GG-DDDT_05August14_03

Scan	Method	Score	m/z
16525	ITMS; ETD	44.1	798.4

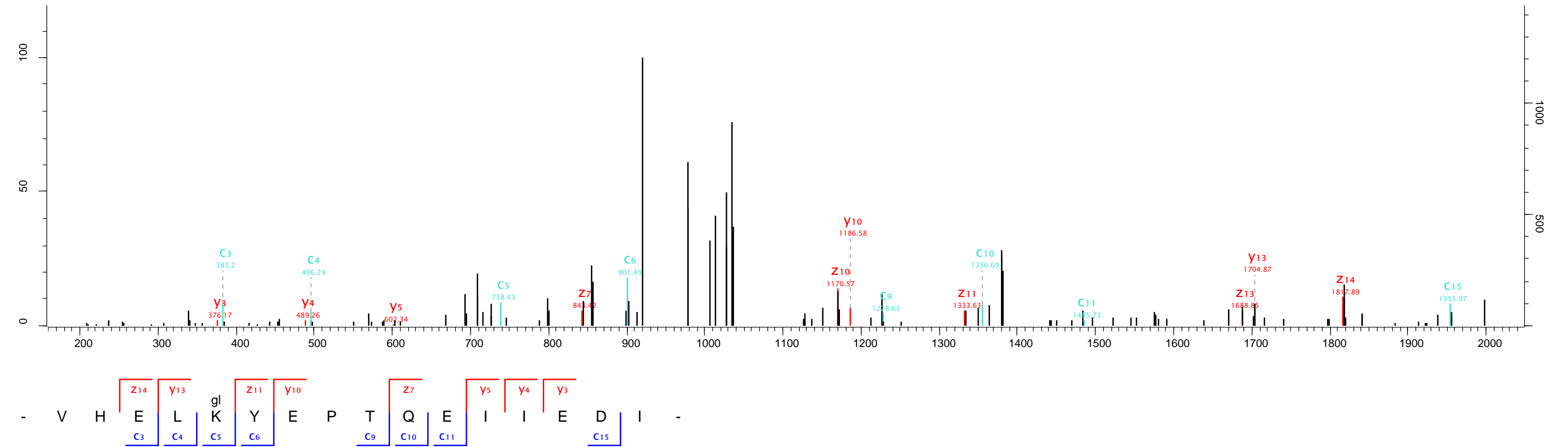


tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03



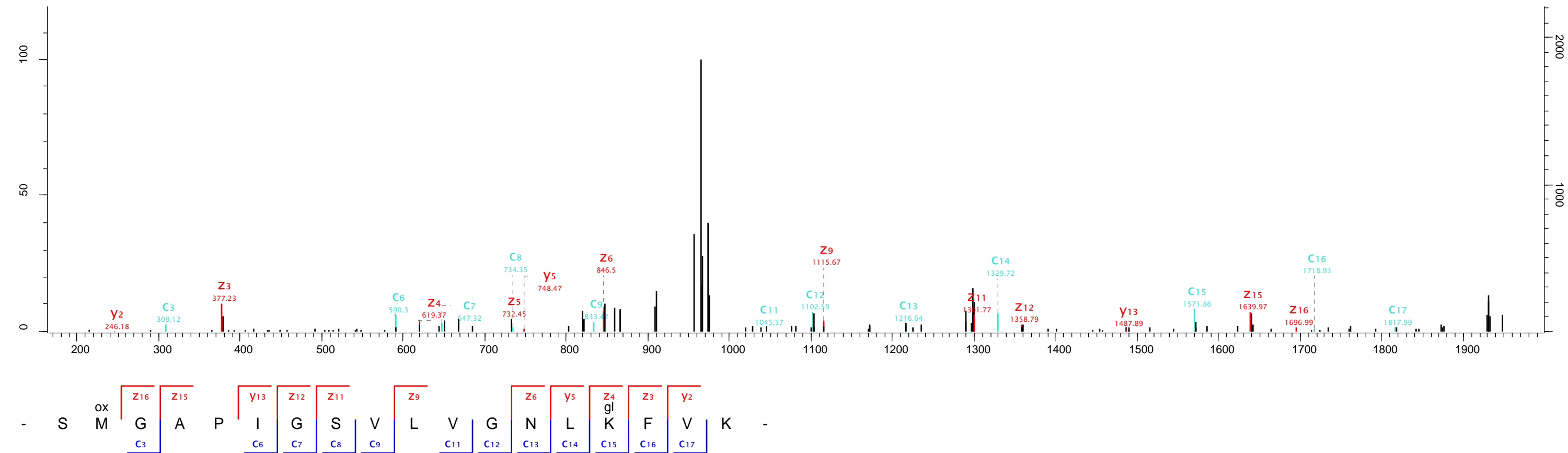
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

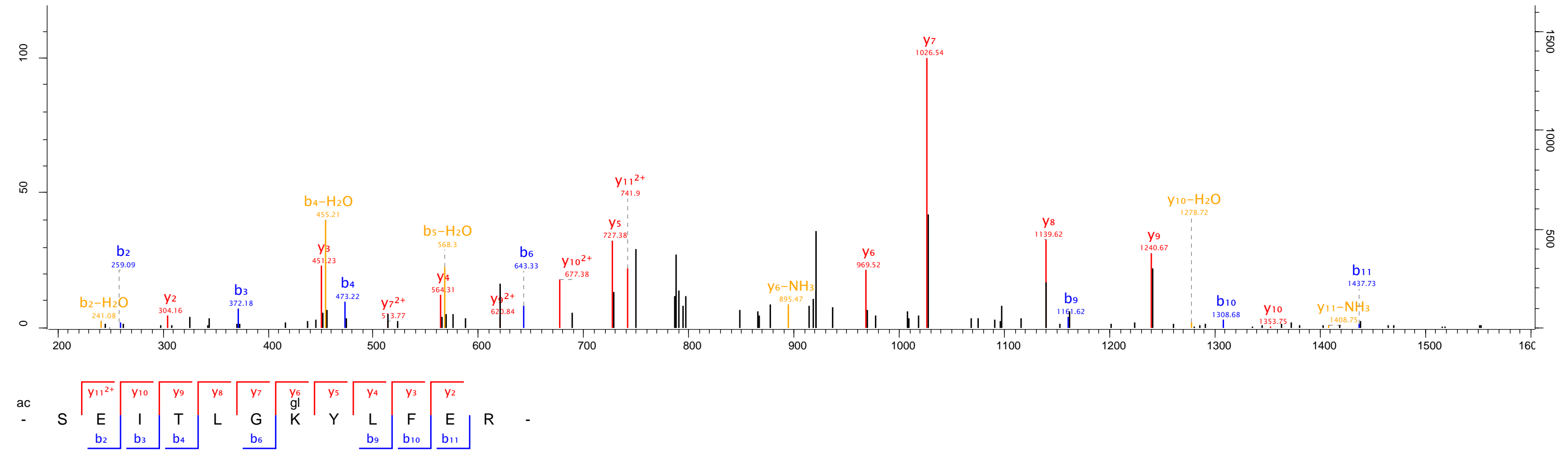
Scan	Method	Score	m/z
18329	ITMS; ETD	189.04	691.02



Scan	Method	Score	m/z
------	--------	-------	-----

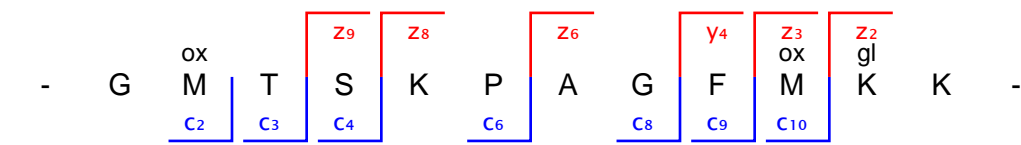
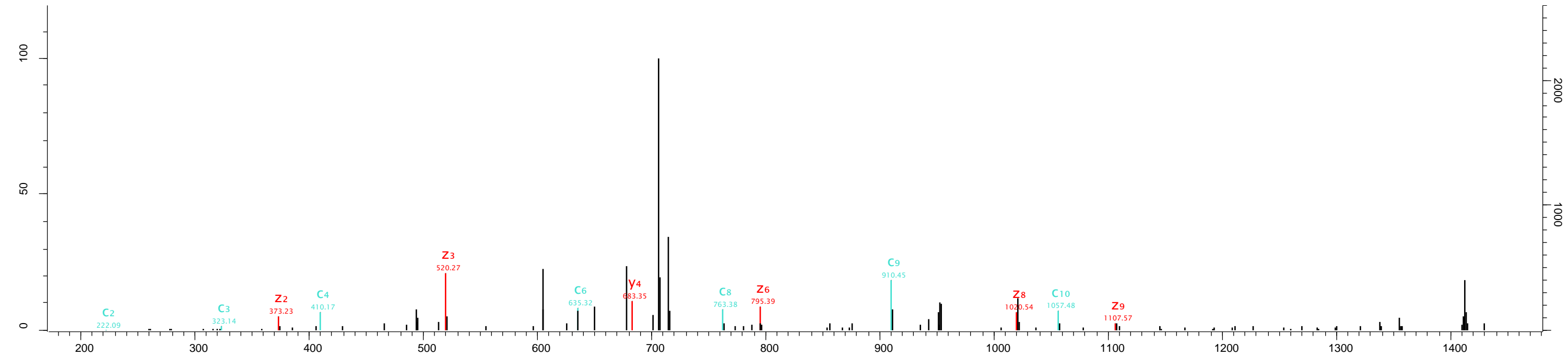
20411	ITMS; ETD	175.49	650.03
-------	-----------	--------	--------





Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

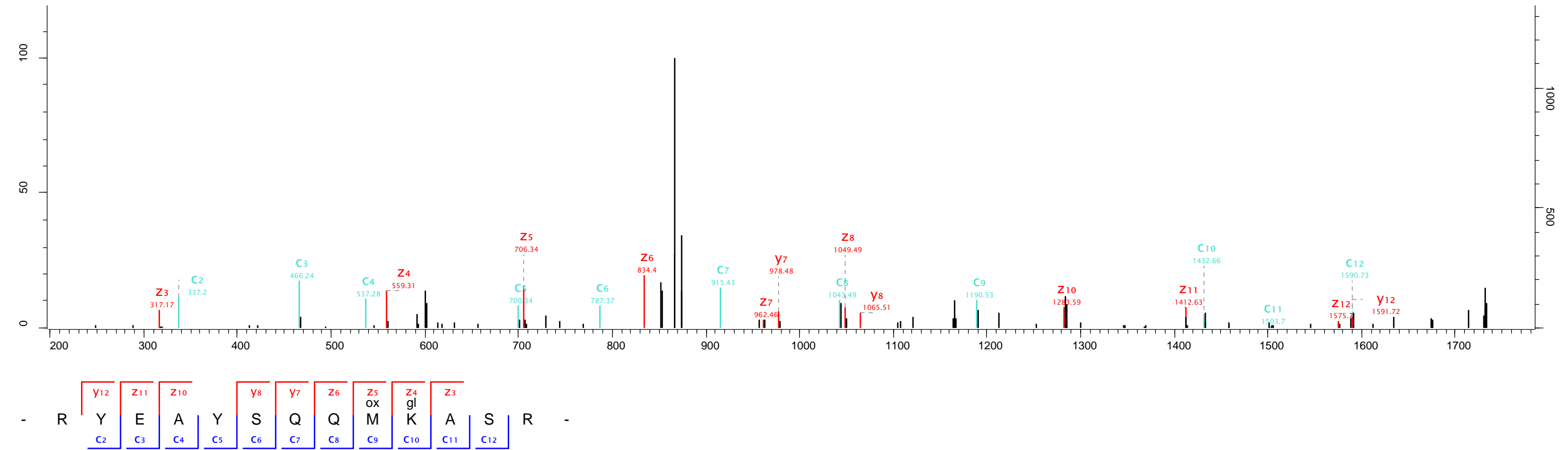
Scan Method Score m/z
352 ITMS; ETD 122.55 476.9



Raw file

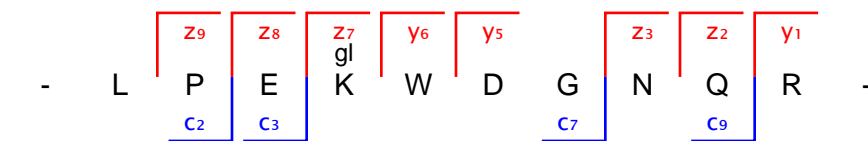
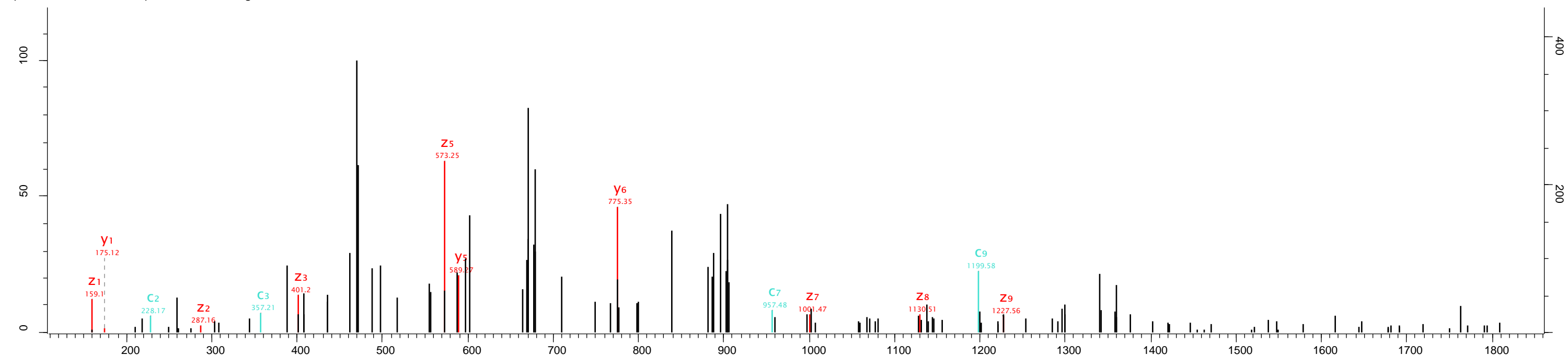
Scan373MethodITMS; ETDScore232.17m/z583.28

tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03



Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

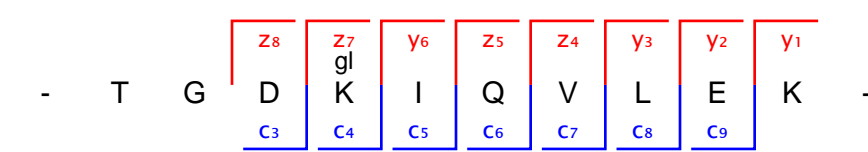
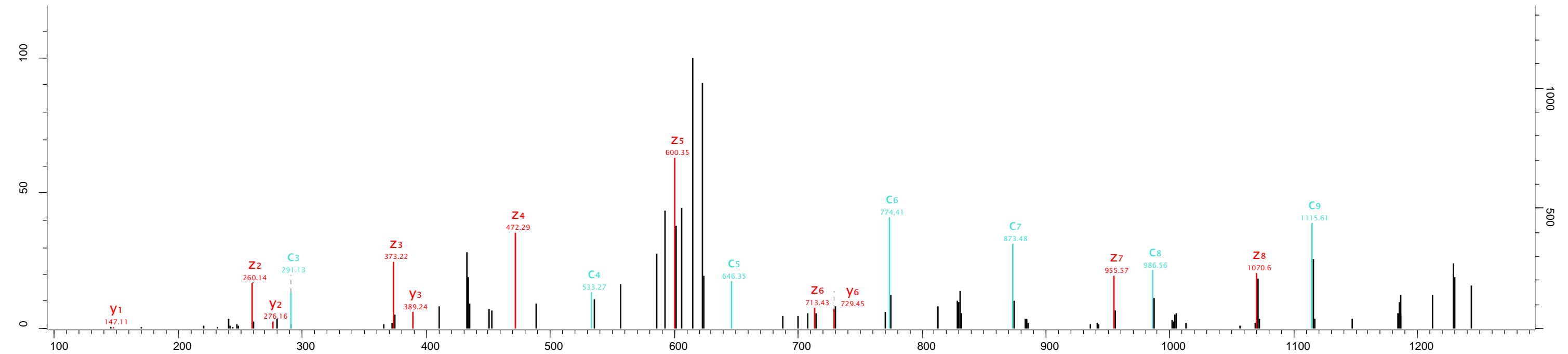
Scan	Method	Score	m/z
4240	ITMS; ETD	104.01	453



Raw file

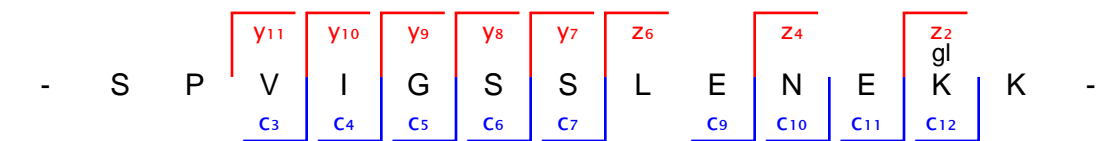
Scan Method Score m/z

tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03 5188 ITMS; ETD 156.01 415.57



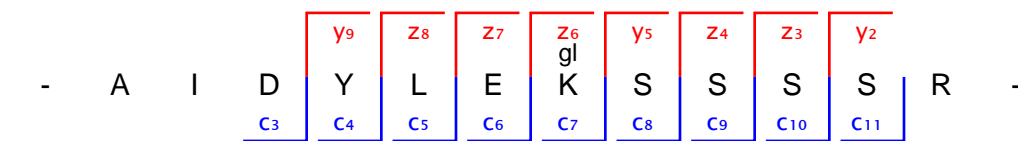
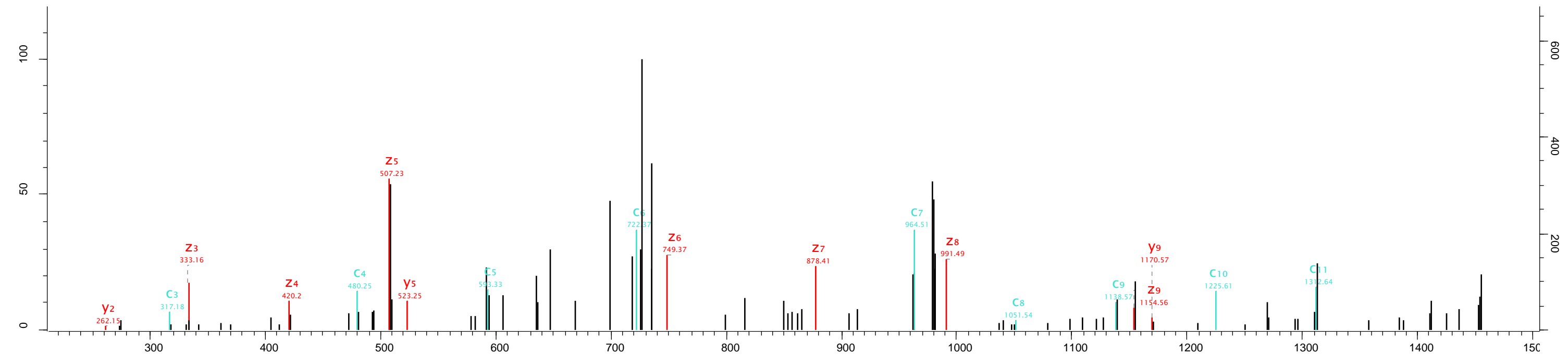
Scan	Method	Score	m/z
------	--------	-------	-----

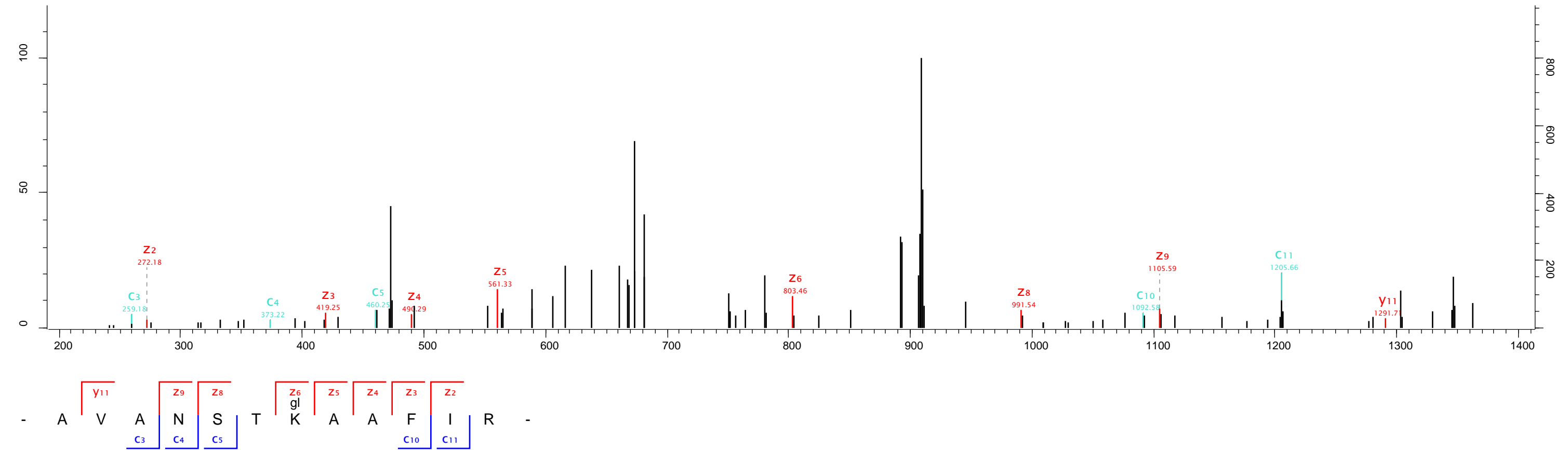
5401	ITMS; ETD	269.14	501.27
------	-----------	--------	--------



tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

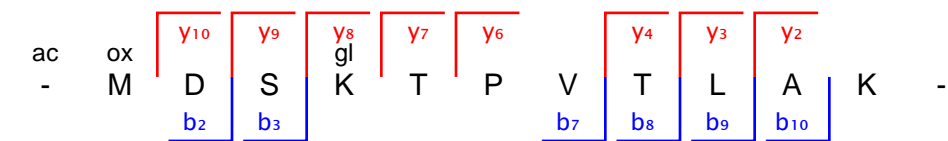
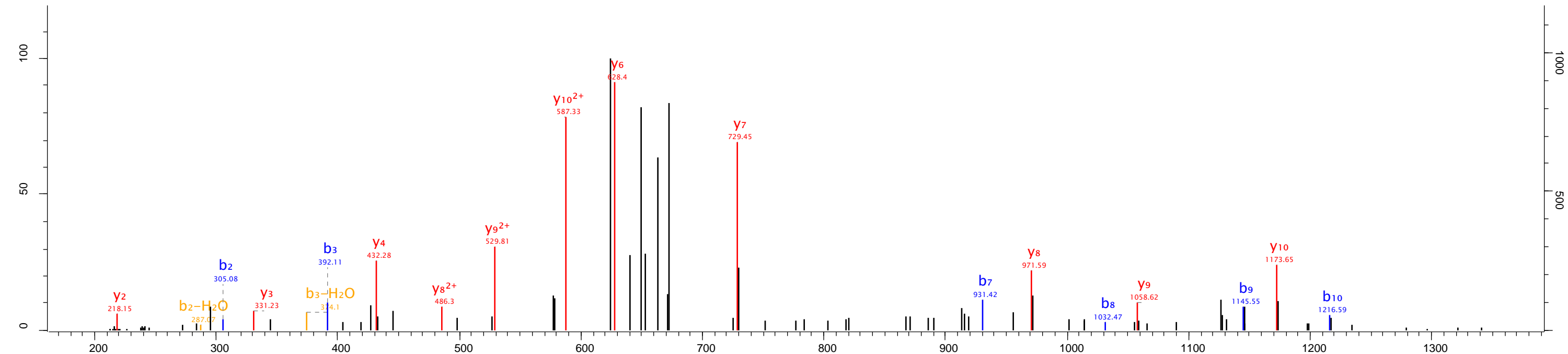
Scan	Method	Score	m/z
5435	ITMS; ETD	149.65	490.58

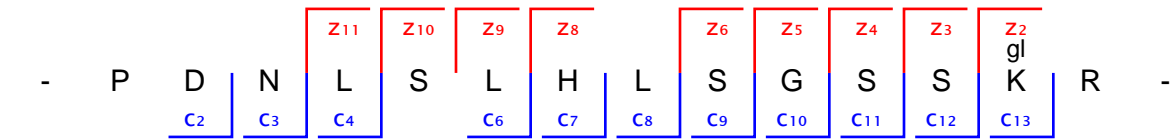
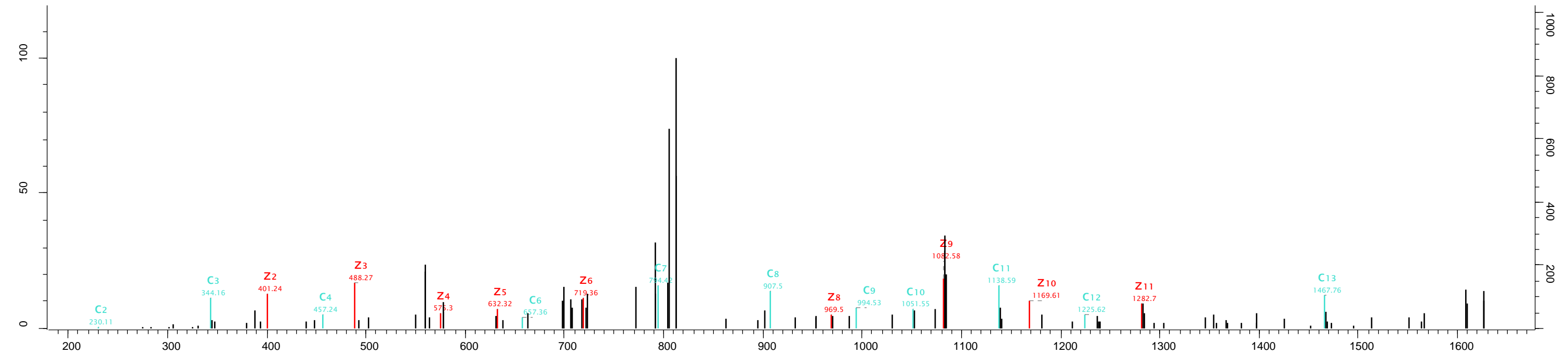


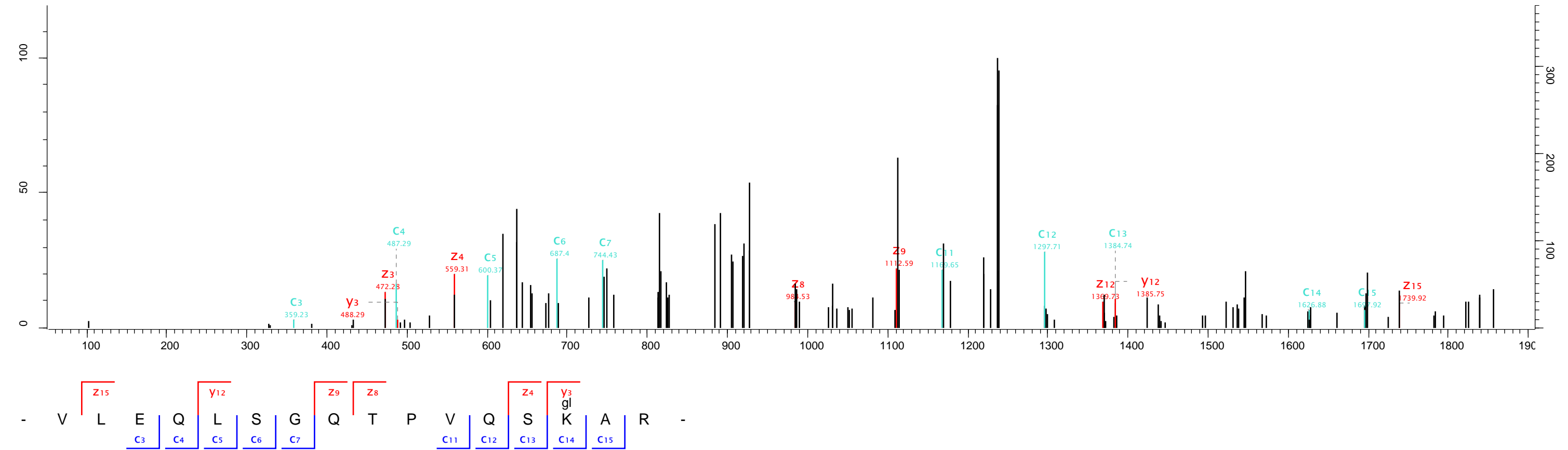


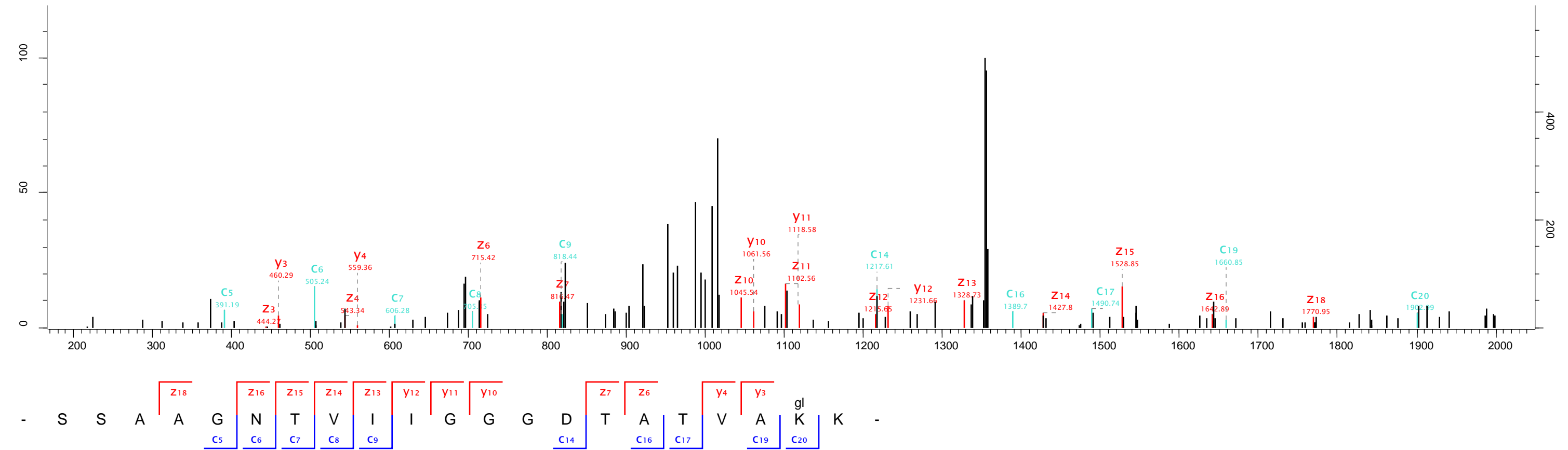
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_05August14_03

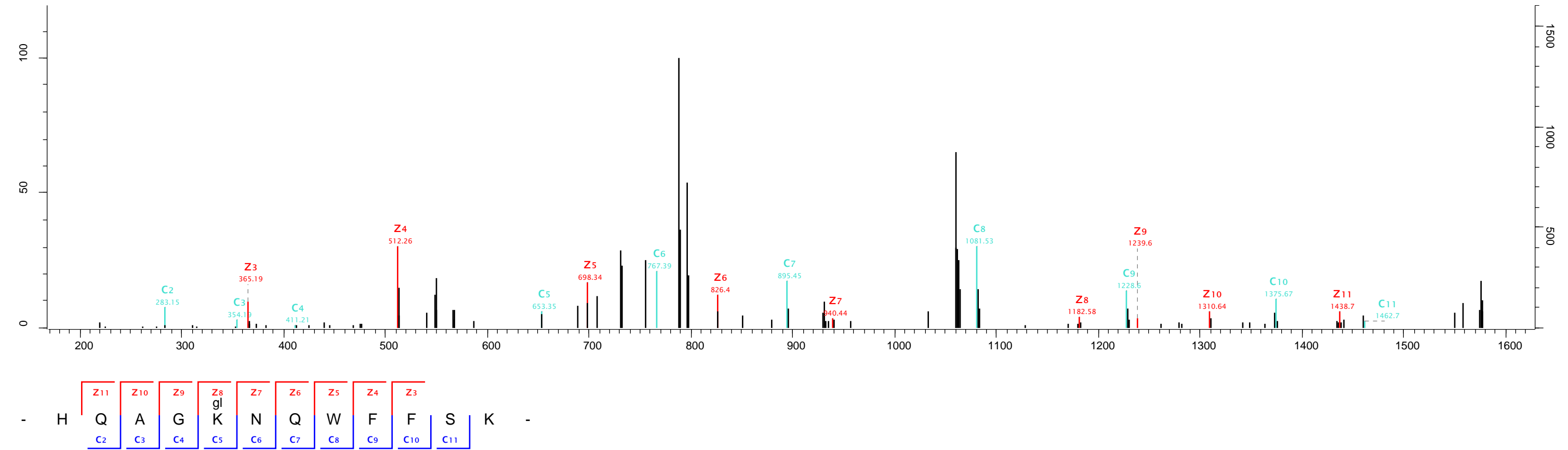
Scan	Method	Score	m/z
6003	ITMS; CID	134.75	681.85

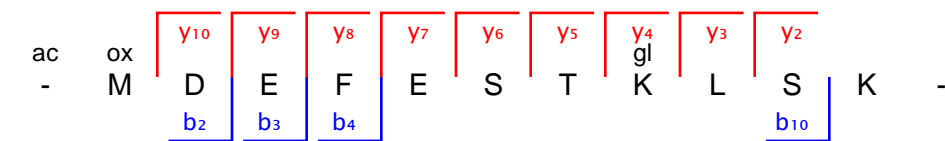
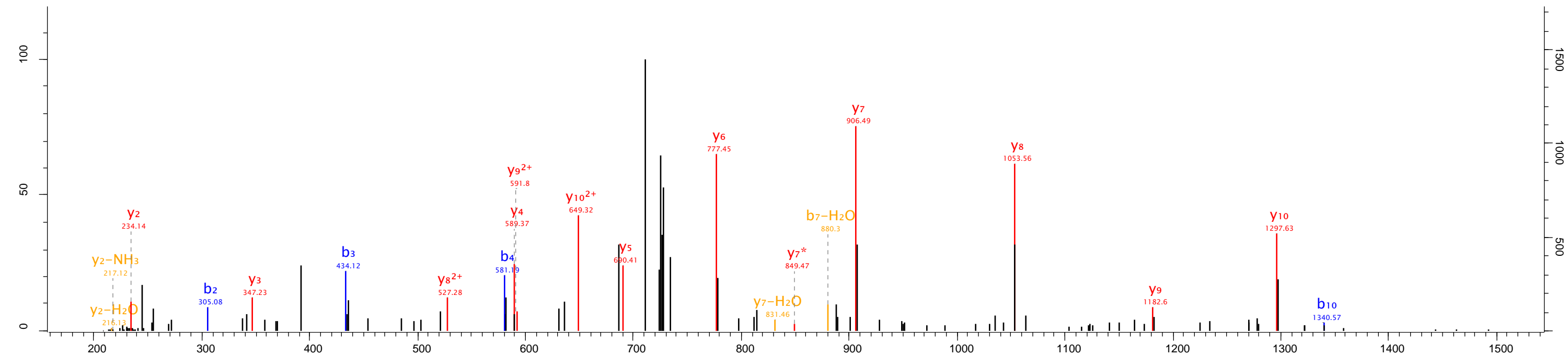


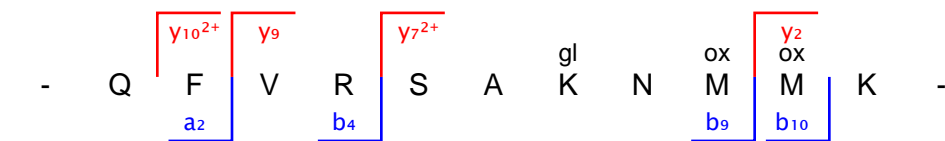
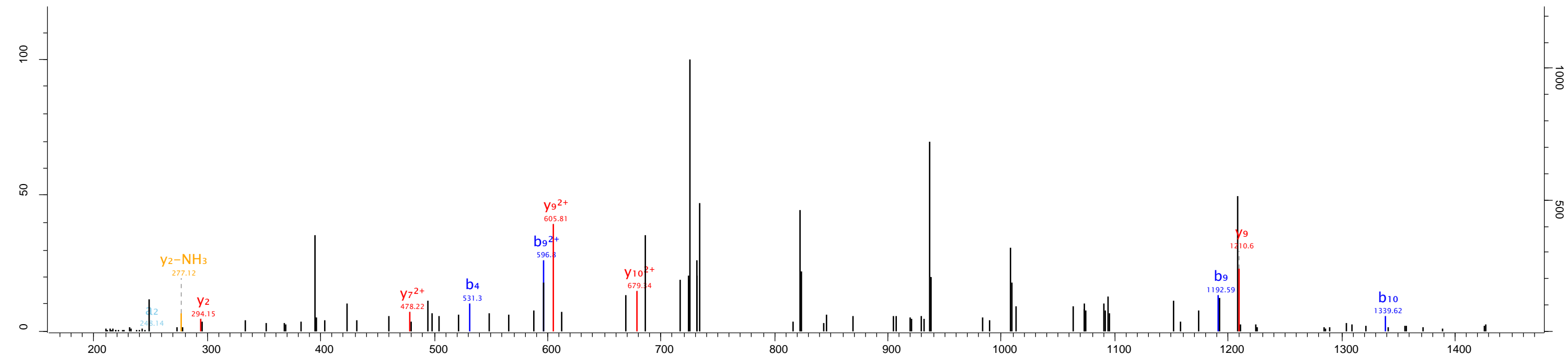


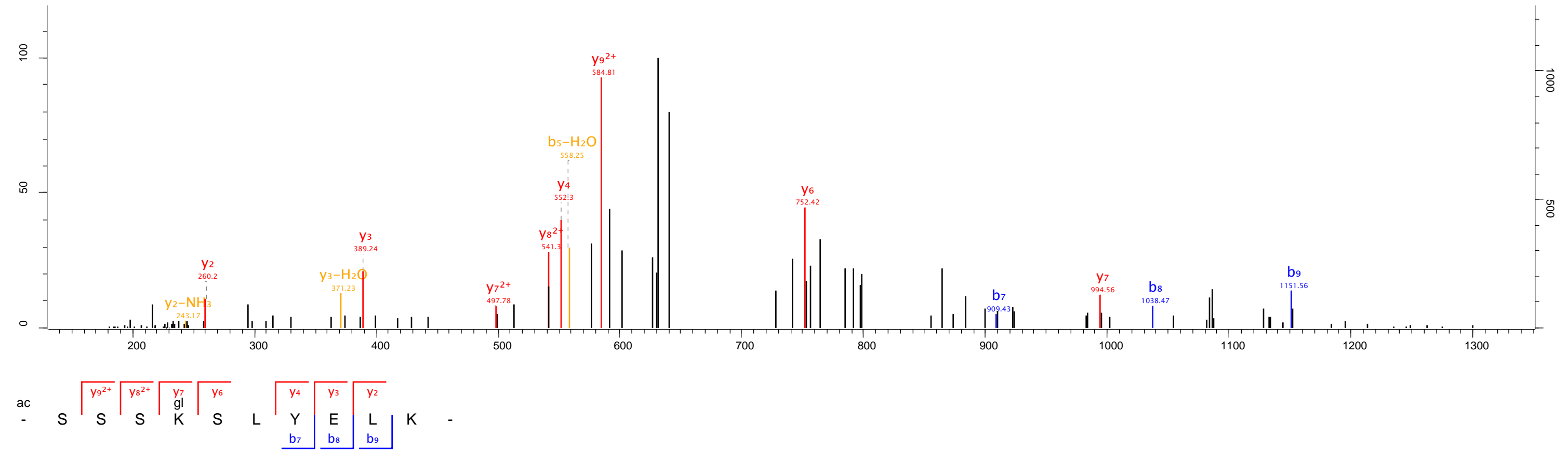


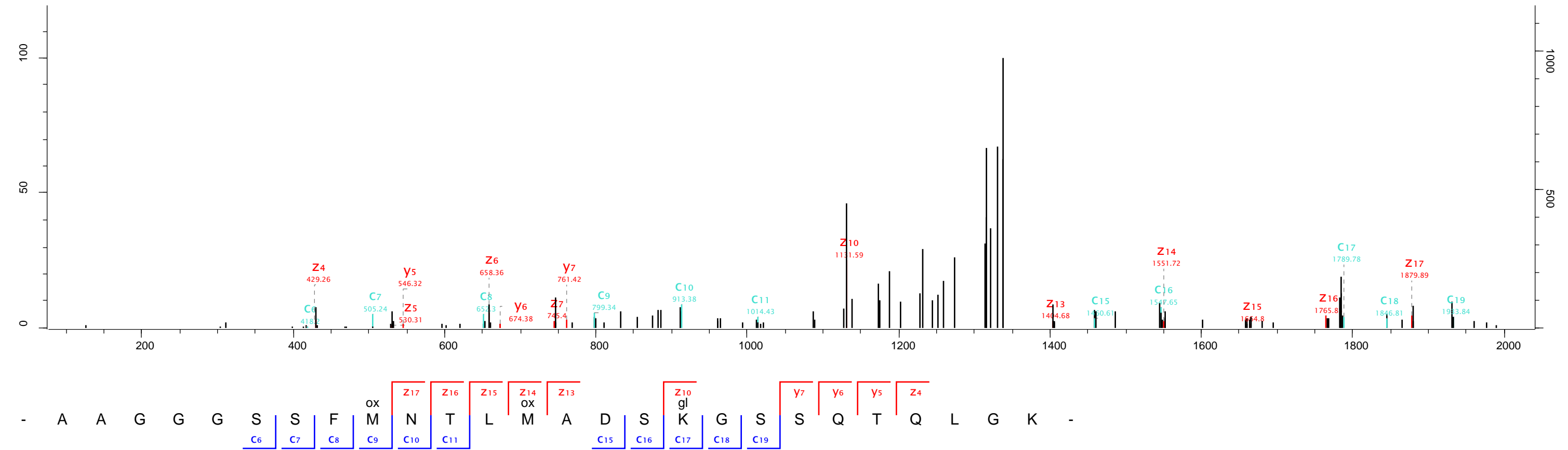


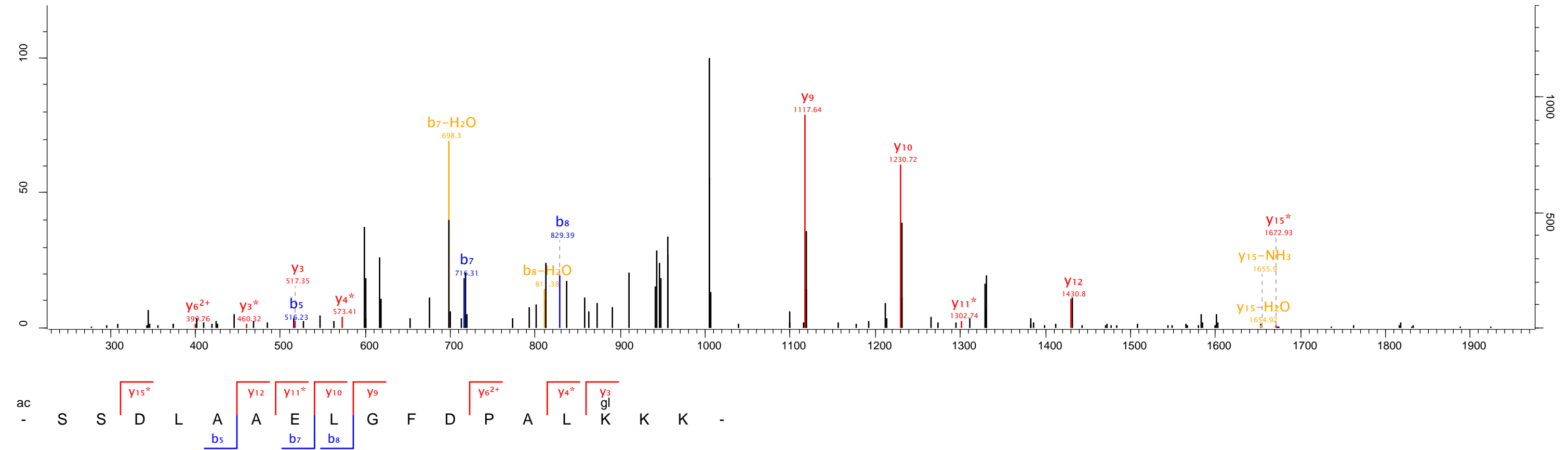






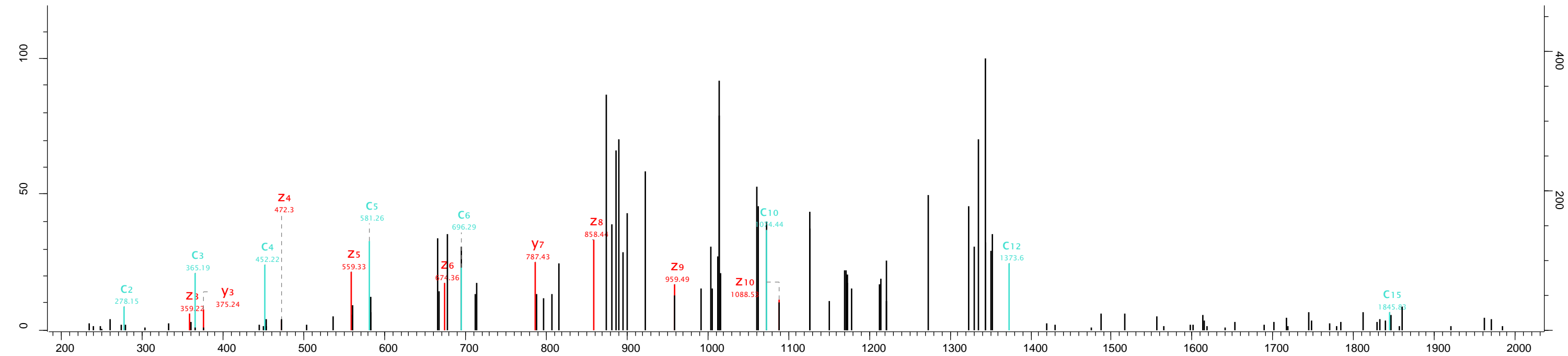






Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

Scan	Method	Score	m/z
10871	ITMS; ETD	87.79	676.82



ox
- M L S S E D F G S S G gl K gl K E T S P D S I S I R -

Peptide sequence: M L S S E D F G S S G K K E T S P D S I S I R

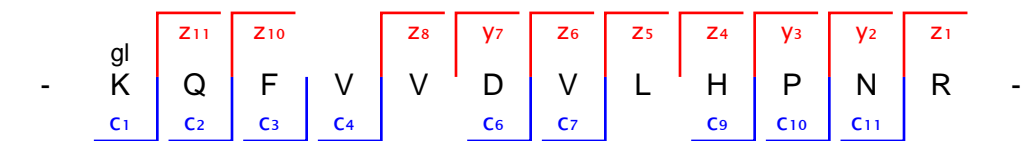
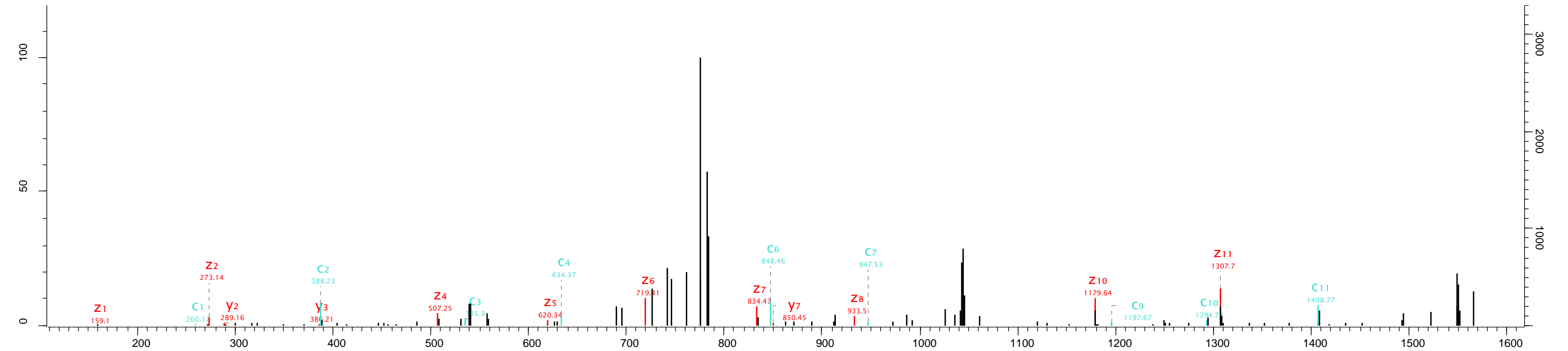
Modifications: Oxidation (ox) on M, Glutathione (gl) on K, Carbamidomethyl (C) on L, S, S, E, D, S, S, G, K, K, E, T, S, P, D, S, I, S, I, R.

Fragmentation sites (indicated by brackets):

- C2 (L)
- C3 (S)
- C4 (S)
- C5 (E)
- C6 (D)
- C10 (S)
- C12 (K)
- C15 (T)
- Z10 (E)
- Z9 (T)
- Z8 (S)
- Y7 (P)
- Z6 (D)
- Z5 (S)
- Z4 (I)
- Y3 (S)

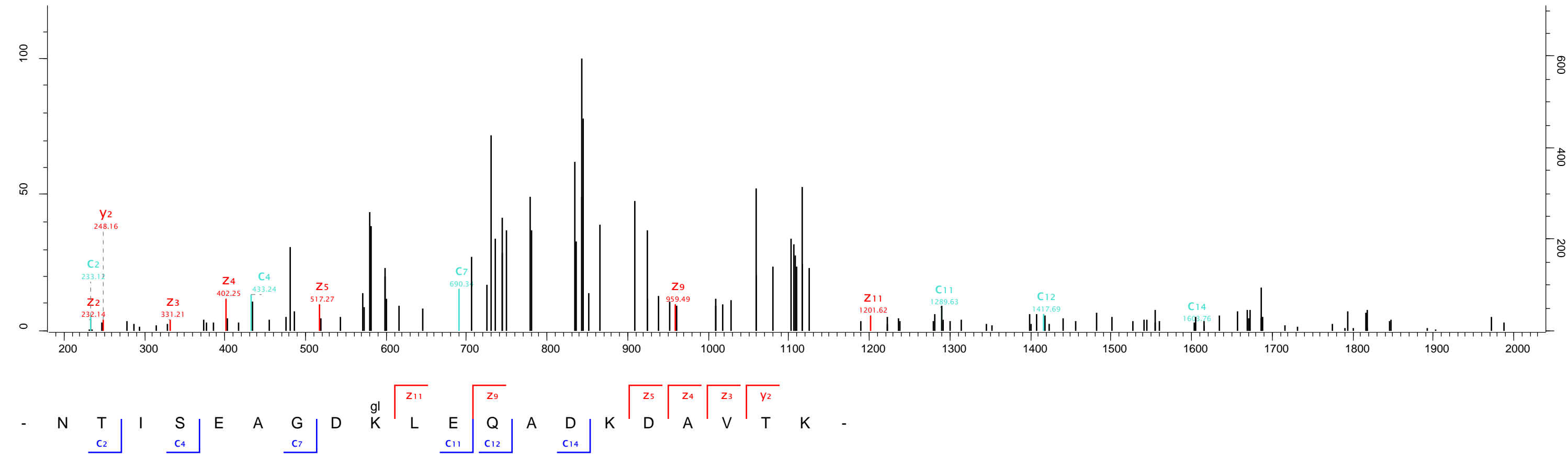
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

Scan	Method	Score	m/z
11048	ITMS; ETD	176.09	522.62



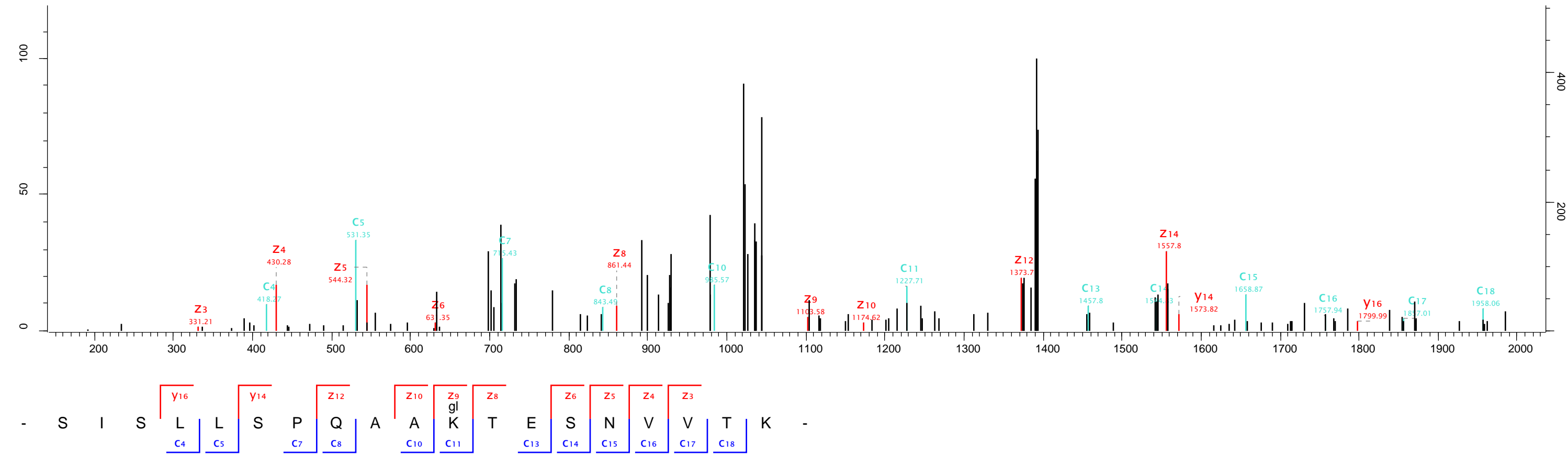
Raw file
tay_Yeast_Untreated_WCLip_GG-DDDT_A_06August14_02

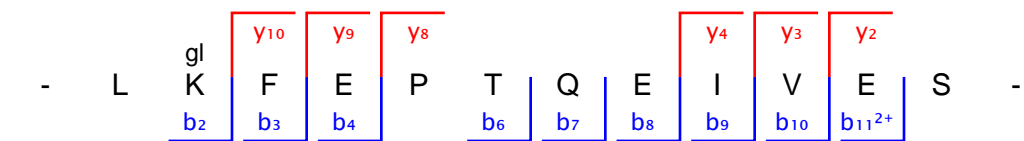
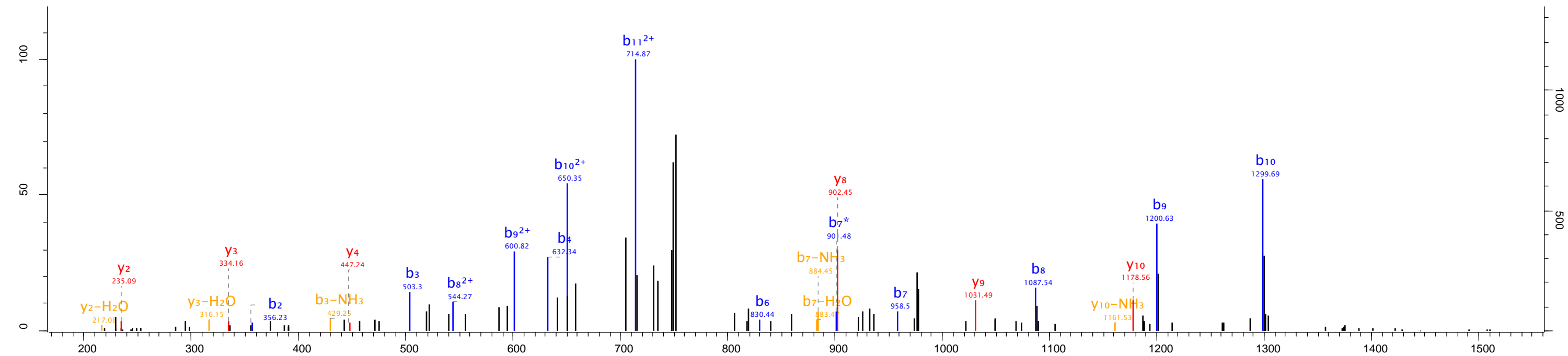
Scan	Method	Score	m/z
12351	ITMS; ETD	74.54	563.04



Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

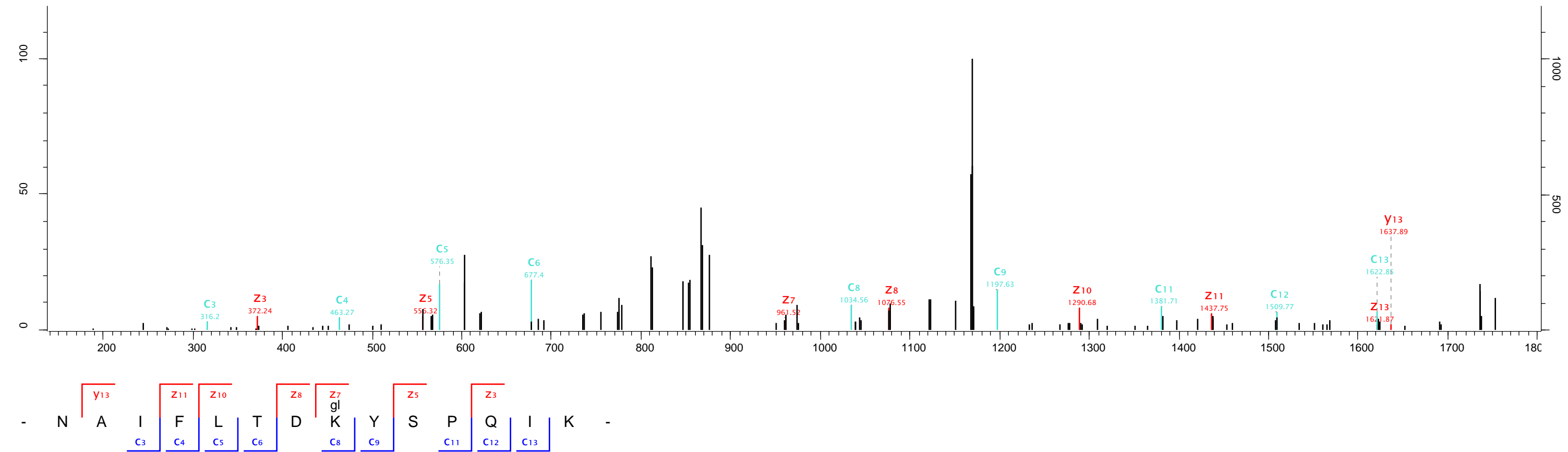
Scan	Method	Score	m/z
14270	ITMS; ETD	170.48	696.72

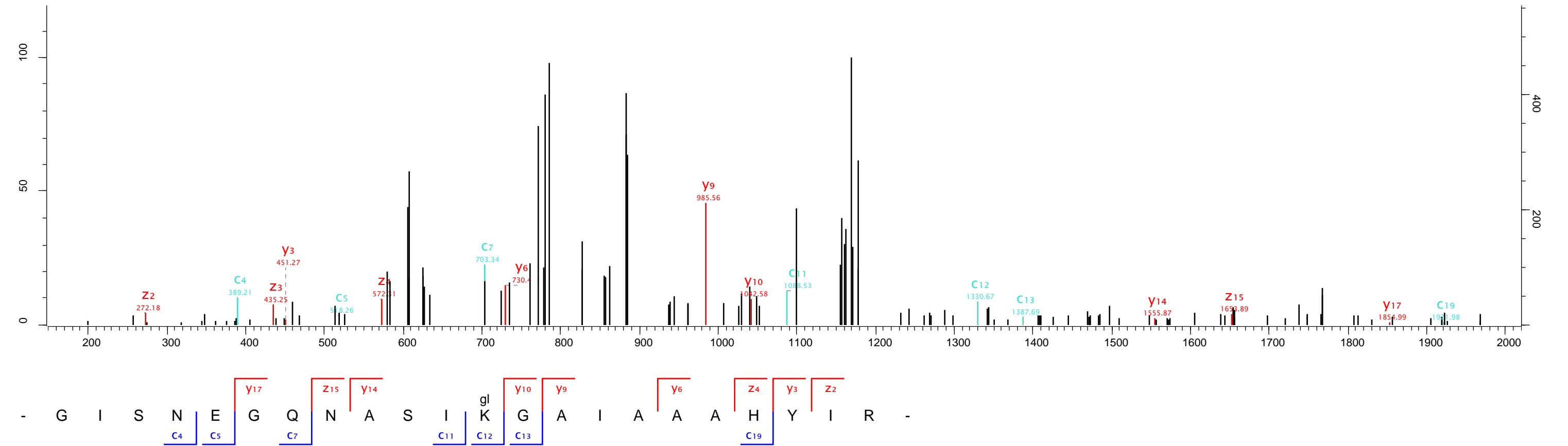


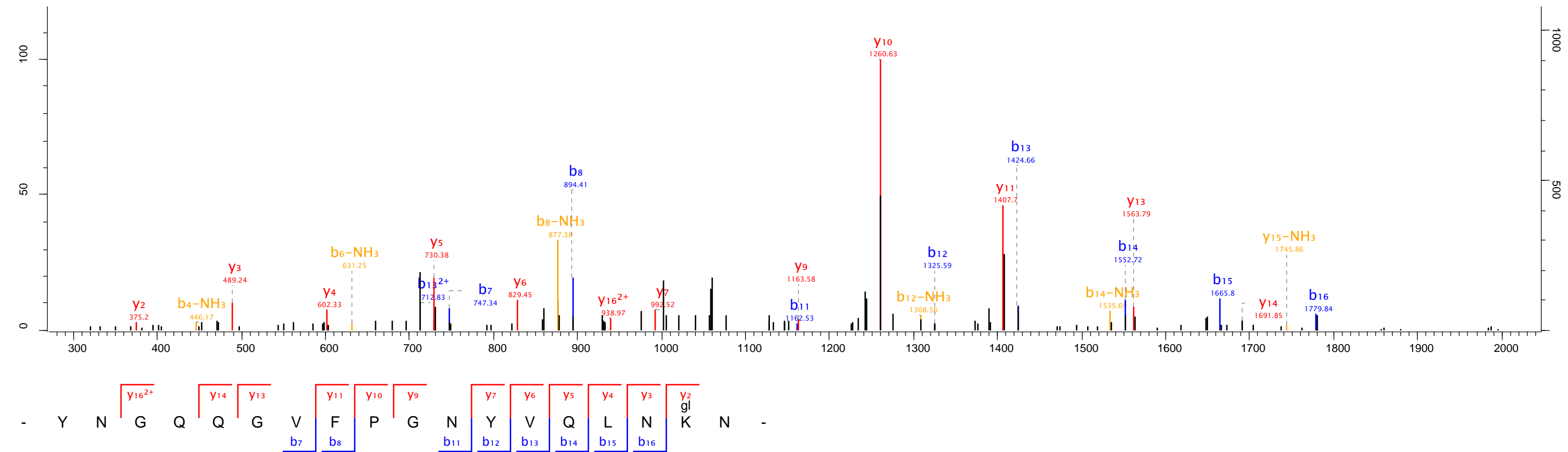


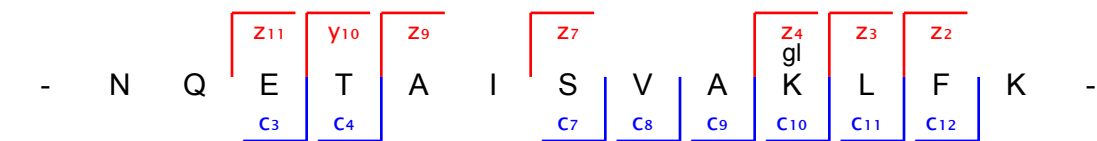
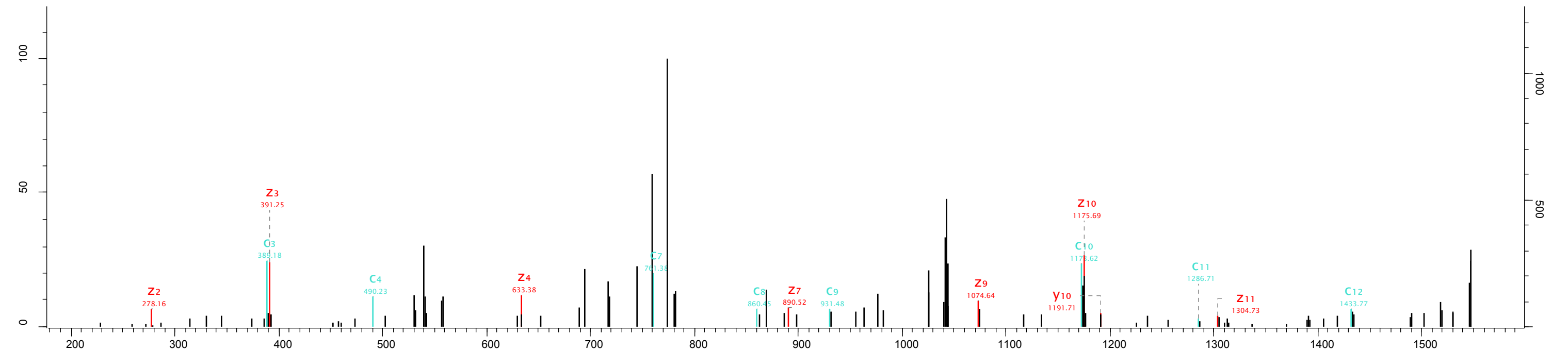
Scan	Method	Score	m/z
------	--------	-------	-----

15260	ITMS; ETD	169.09	584.98
-------	-----------	--------	--------



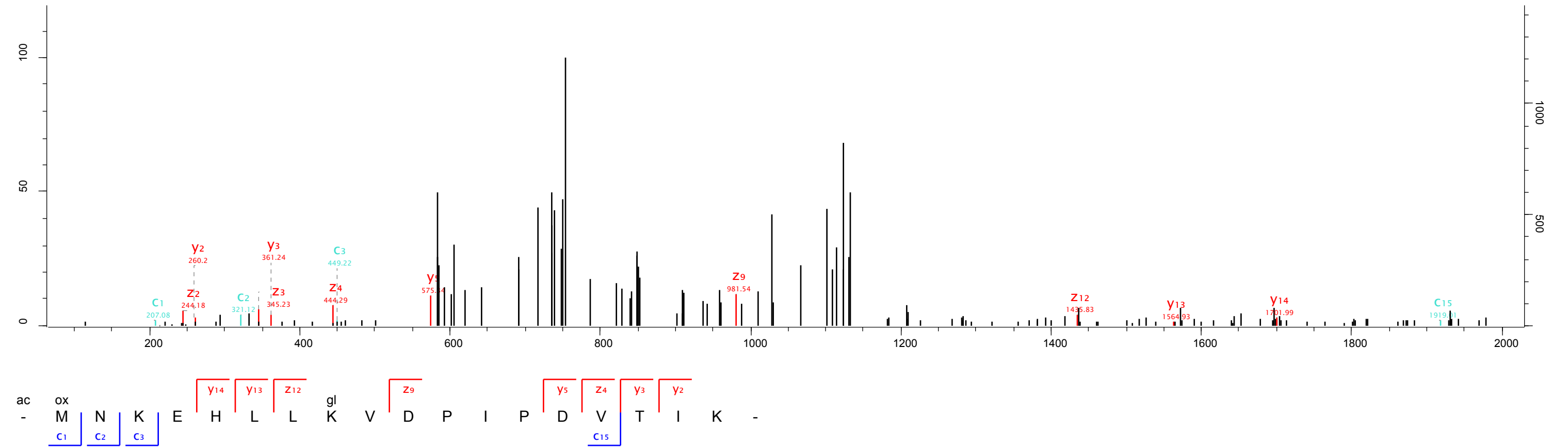


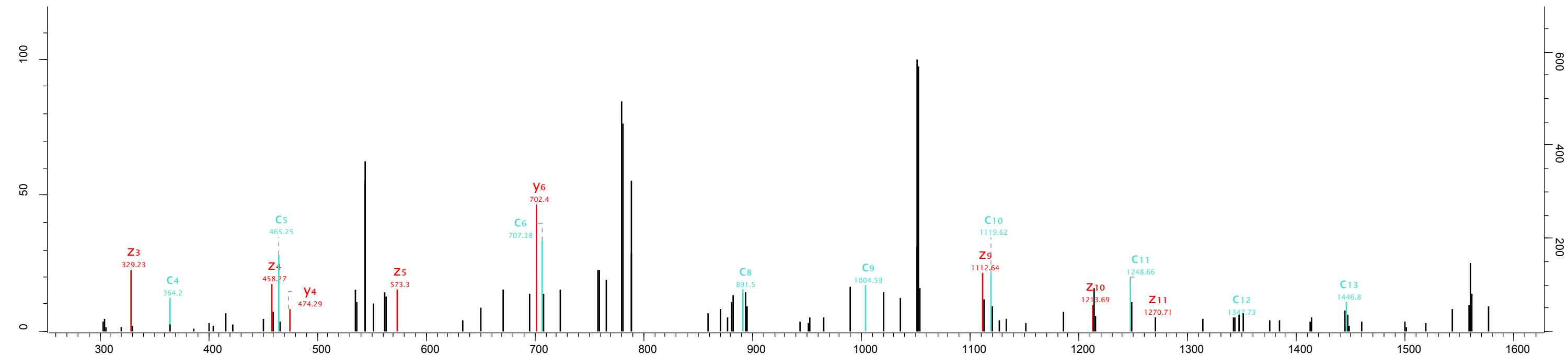




Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

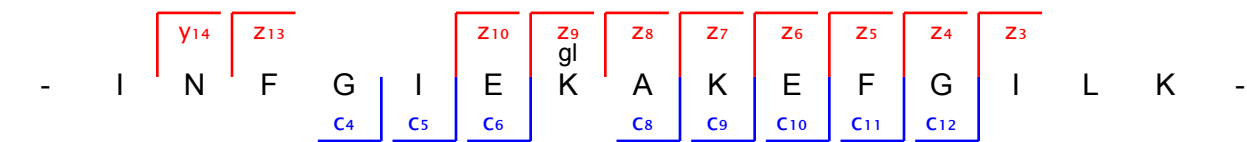
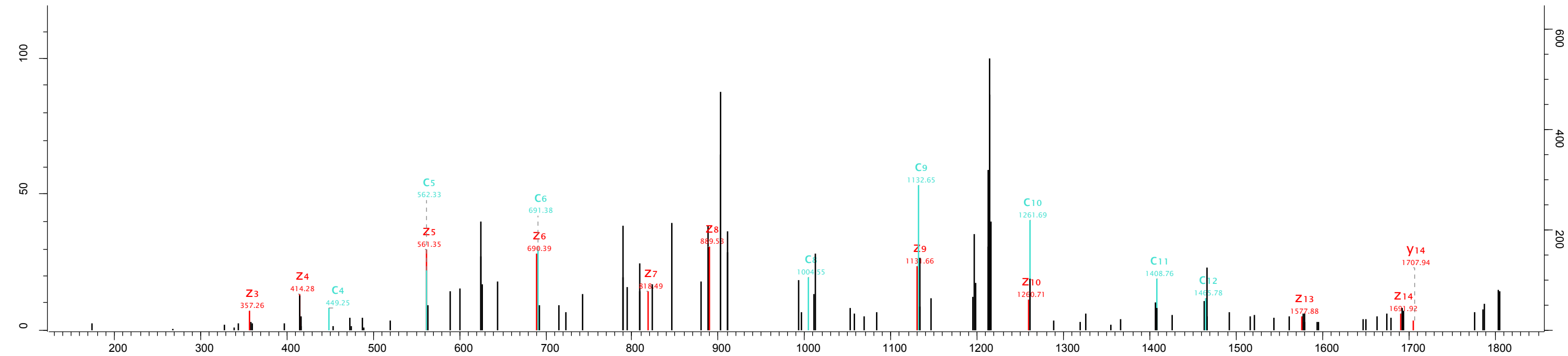
Scan	Method	Score	m/z
17192	ITMS; ETD	70.5	566.56

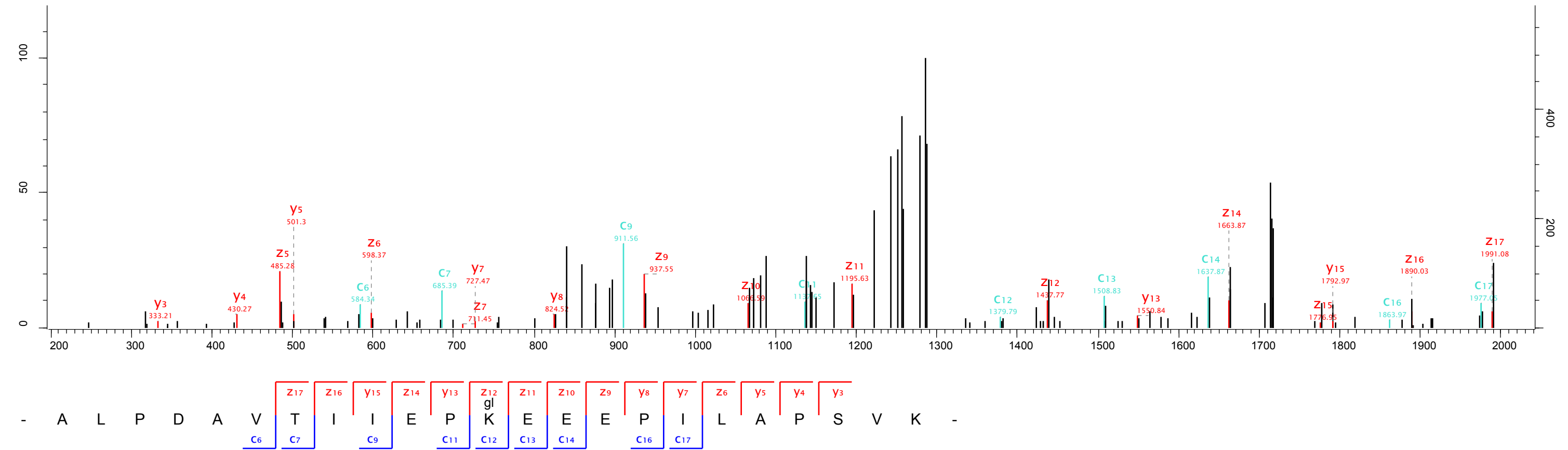


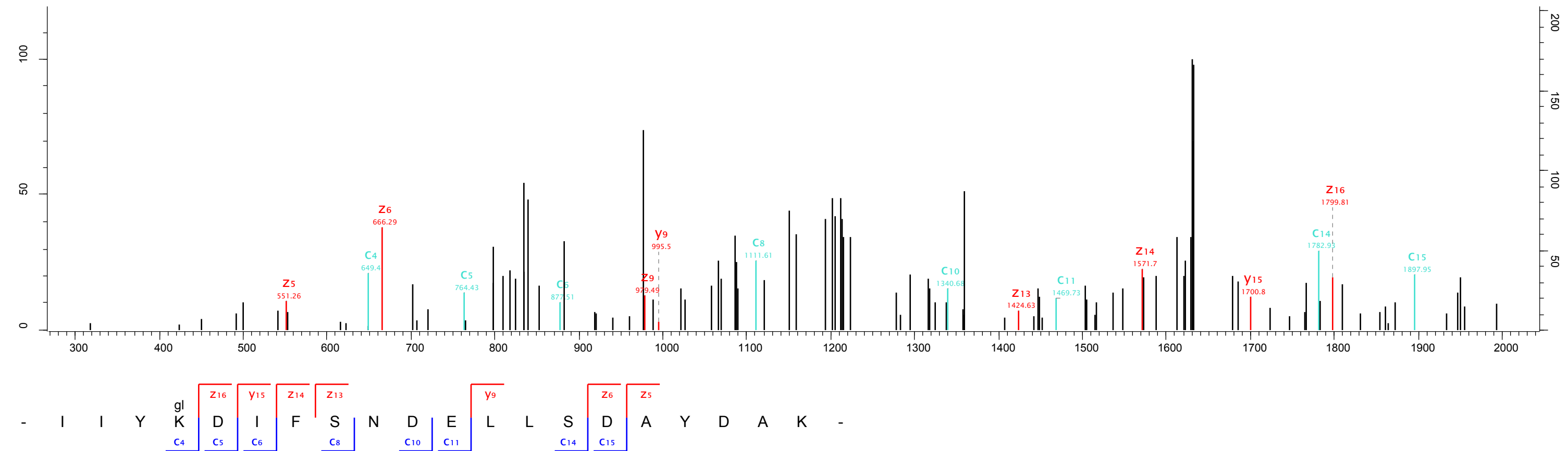


Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

Scan	Method	Score	m/z
18581	ITMS; ETD	119.62	607.68

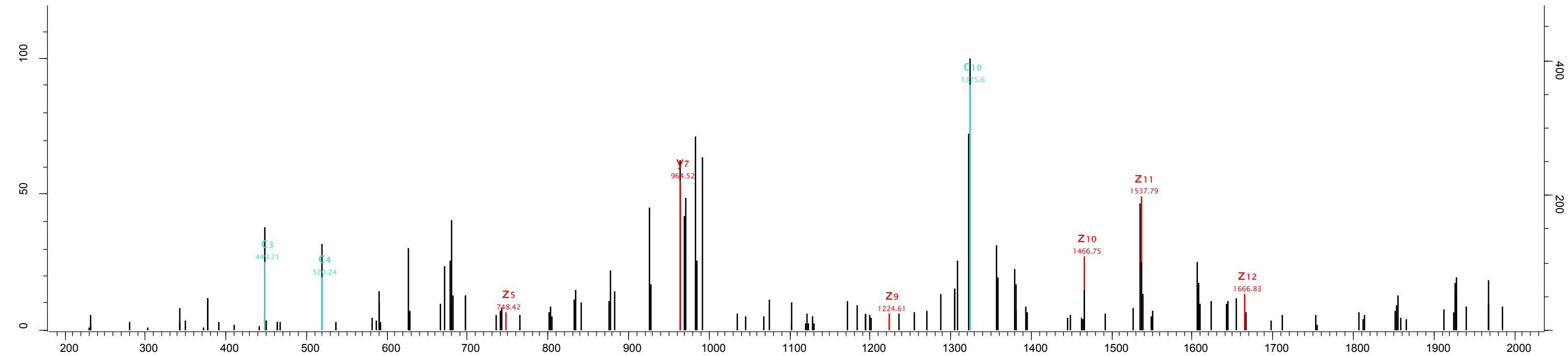






Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

Scan	Method	Score	m/z
23589	ITMS; ETD	54.81	662.33

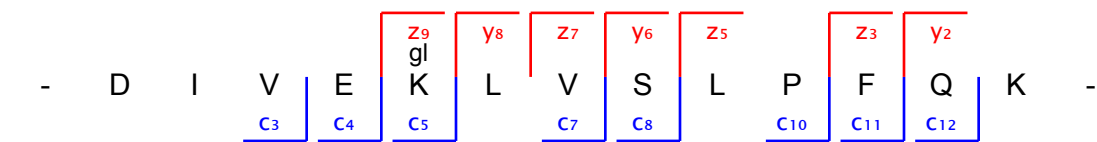
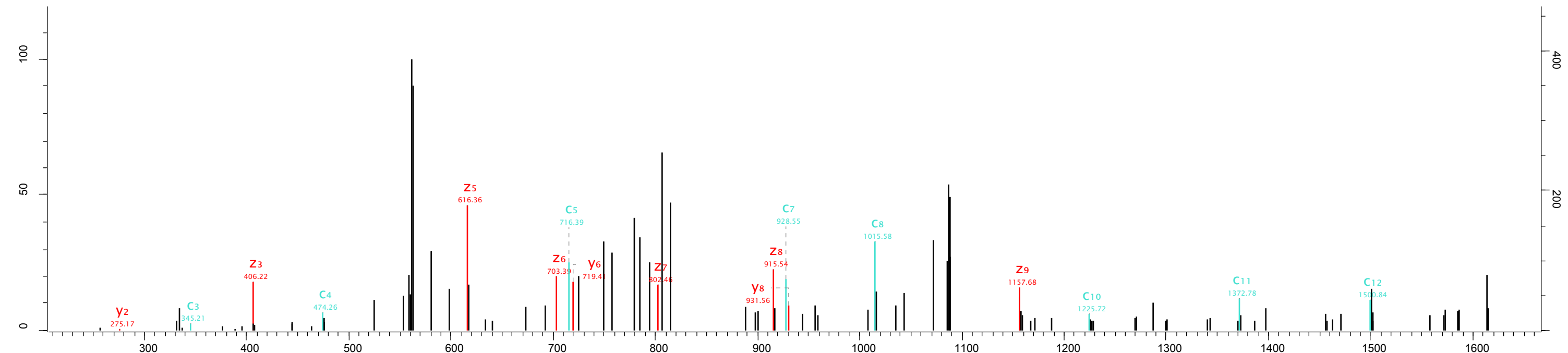


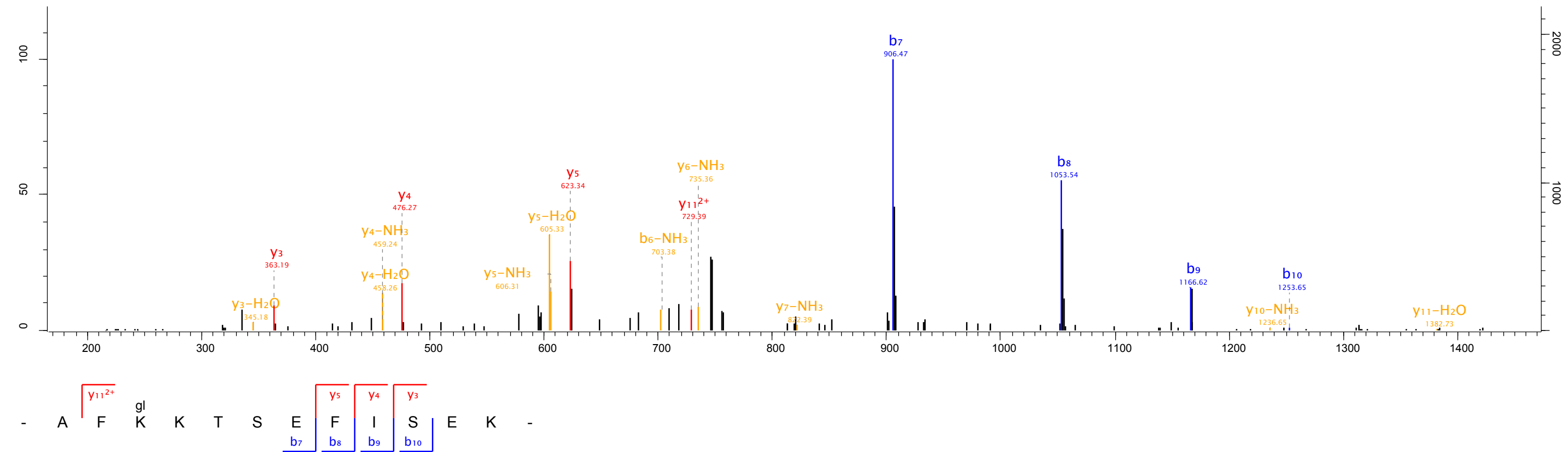
ac ox
- M L

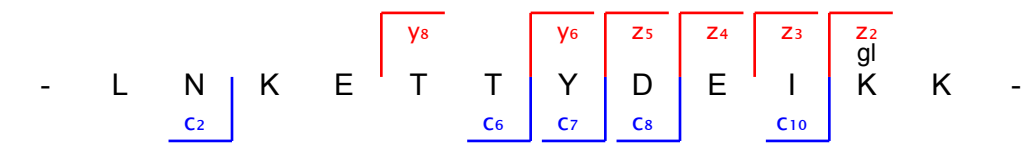
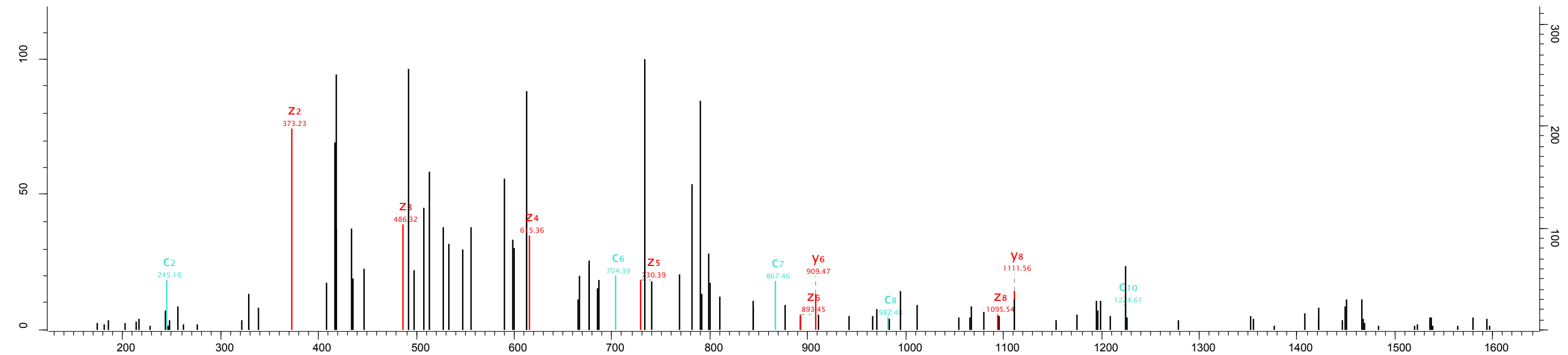
Peptide sequence: E A K F E A S L F K R -

Charge state labels (red): Z12, Z11, Z10, Z9, Y7, Z5

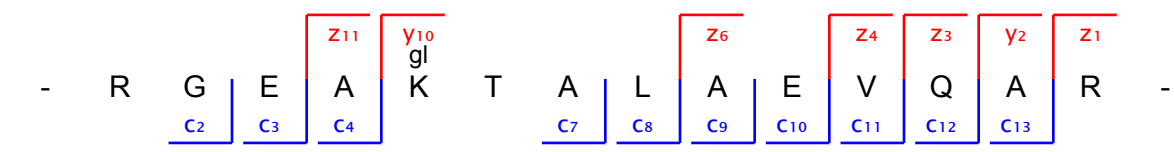
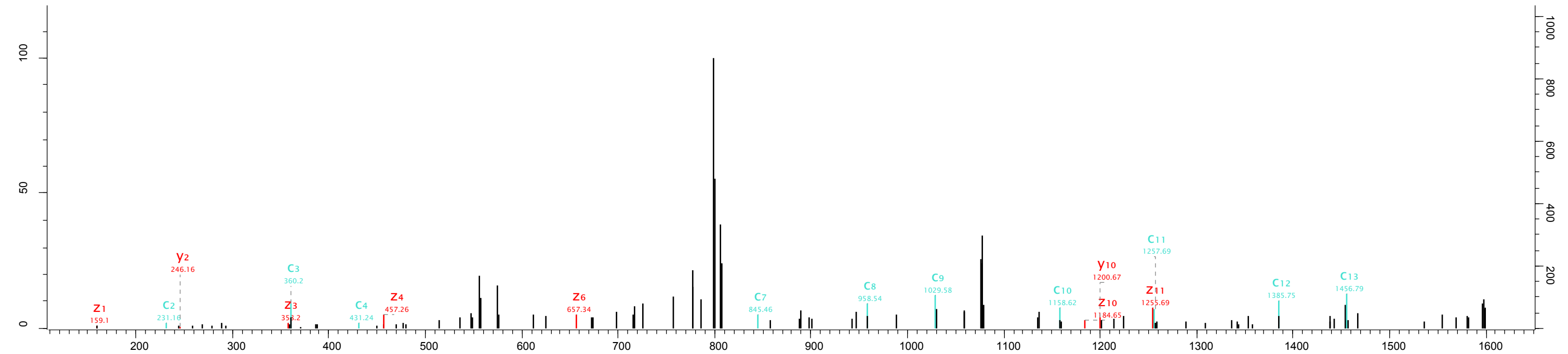
Charge state labels (blue): C3, C4, C10





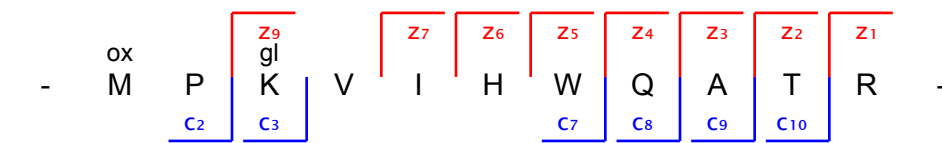
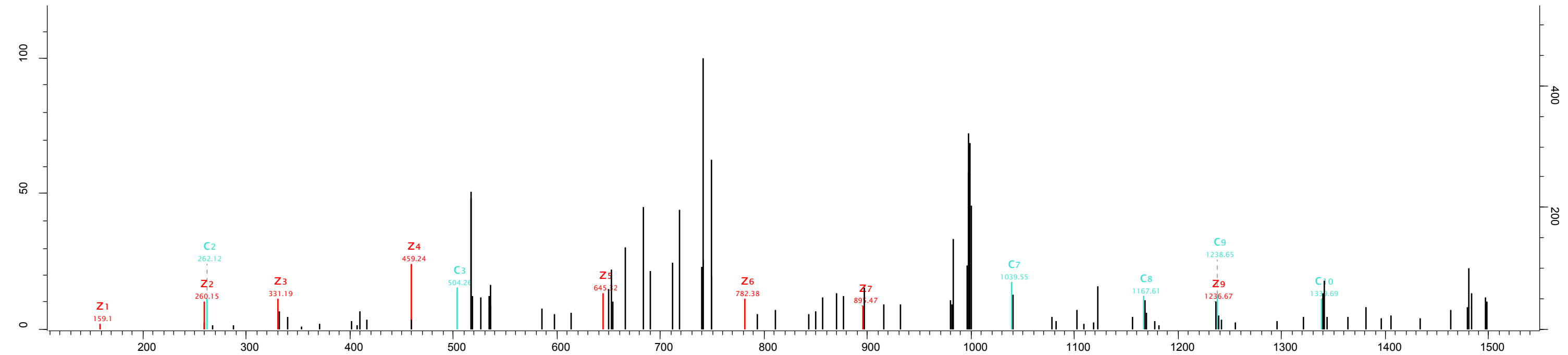


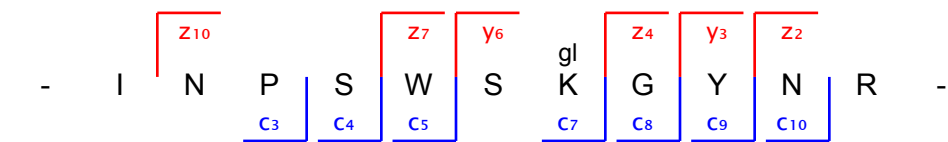
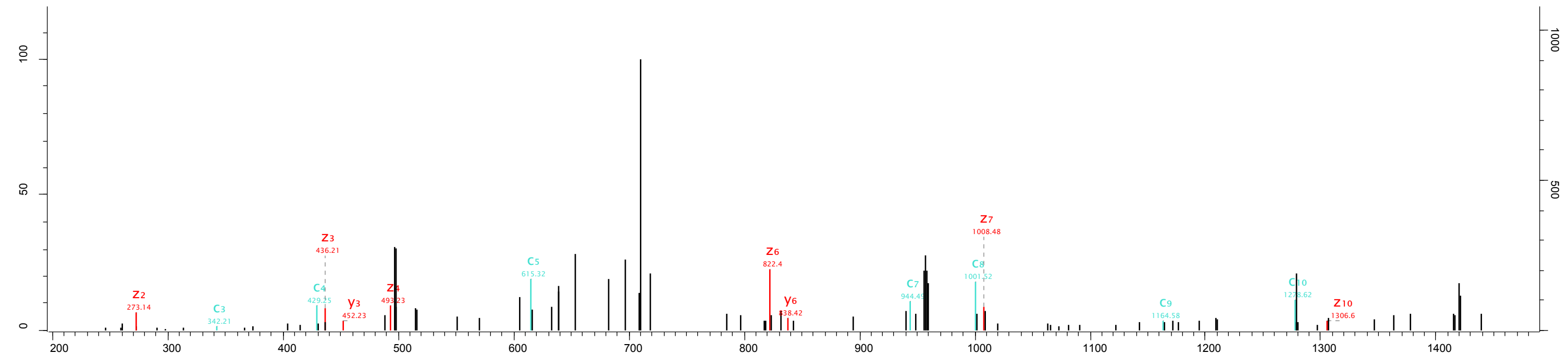
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

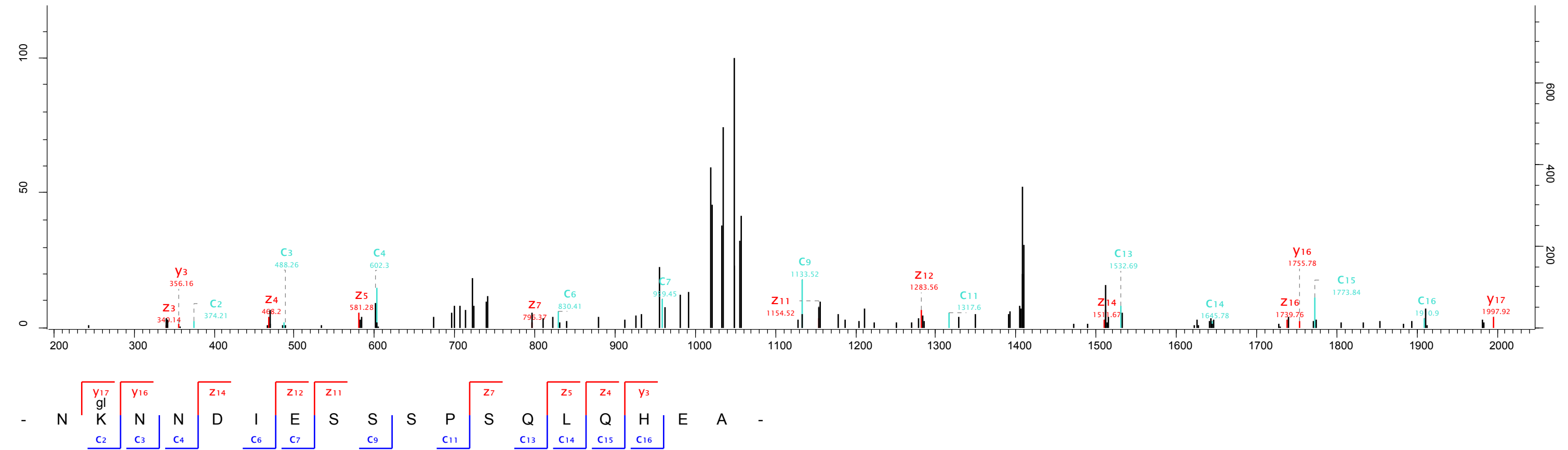


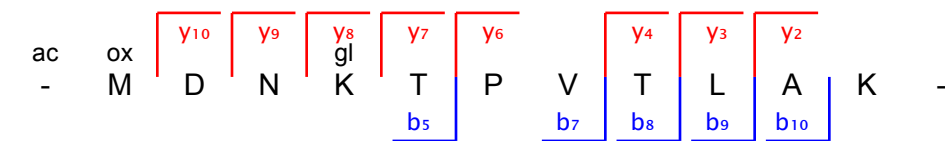
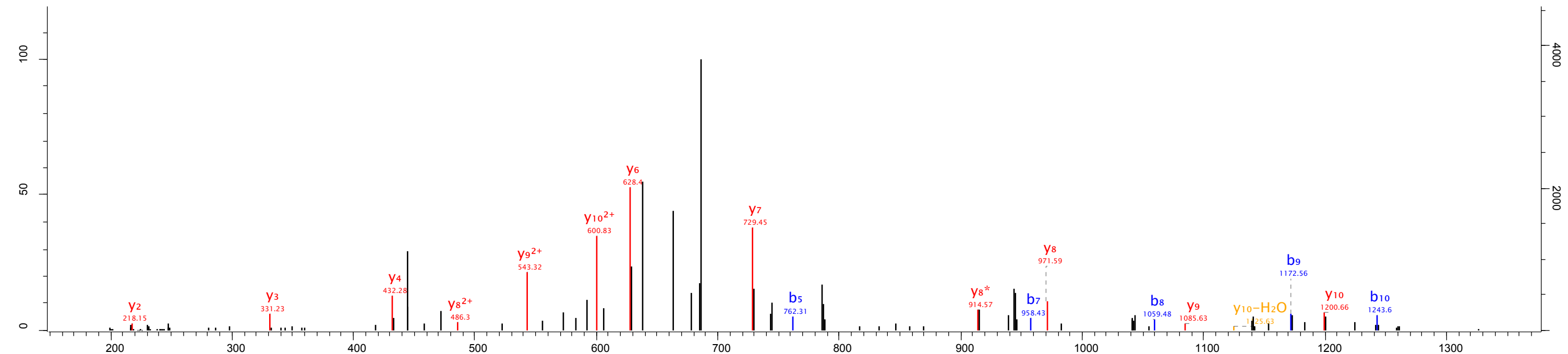
tay_Yeast_Untreated_WCLip_GG-DDDT_A_06August14_02

Scan	Method	Score	m/z
5646	ITMS; ETD	159.04	499.6



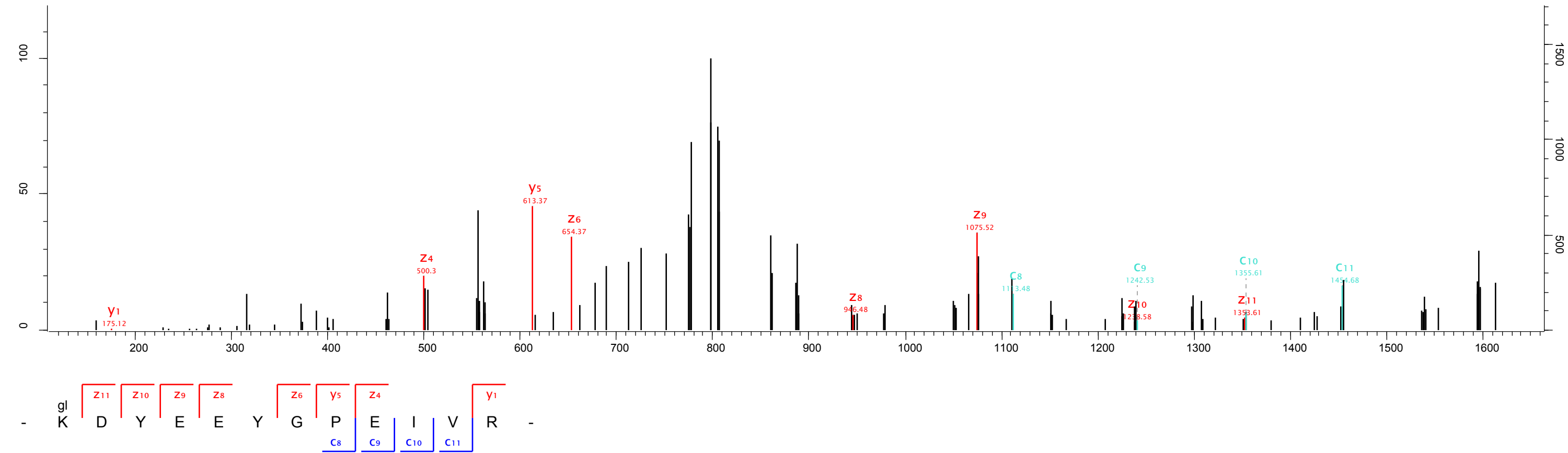






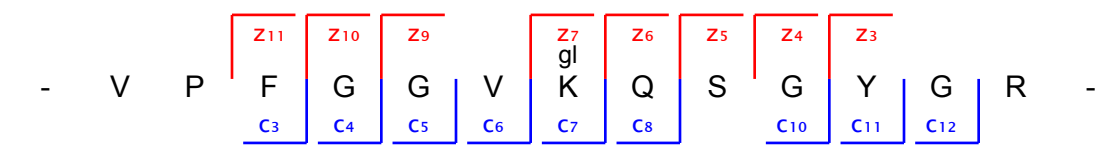
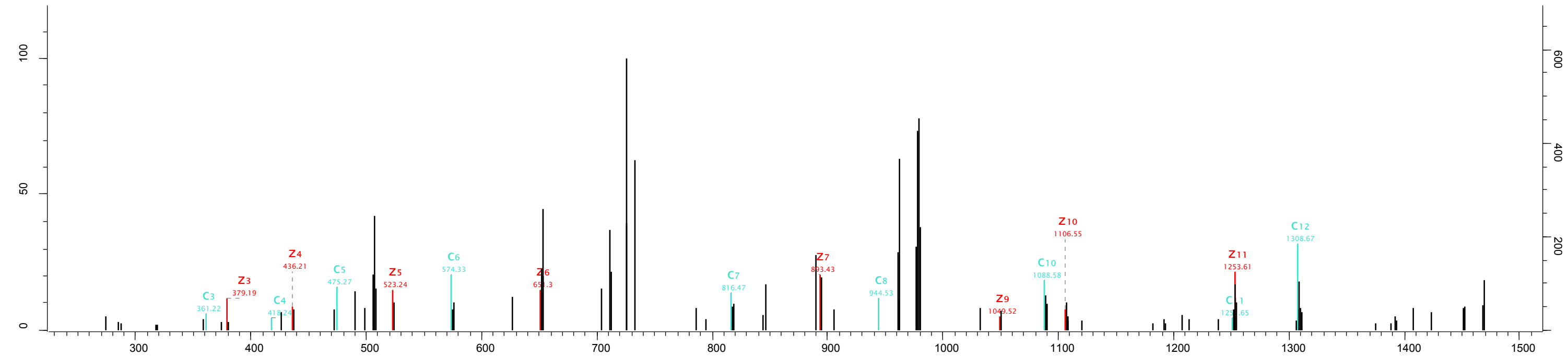
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

Scan	Method	Score	m/z
6901	ITMS; ETD	77.74	538.31



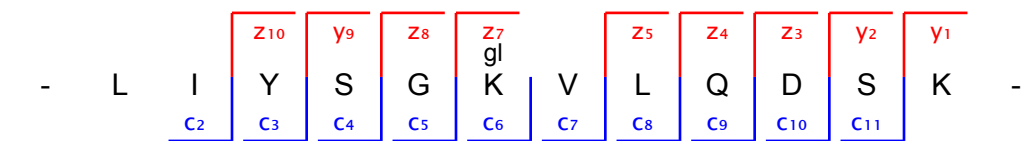
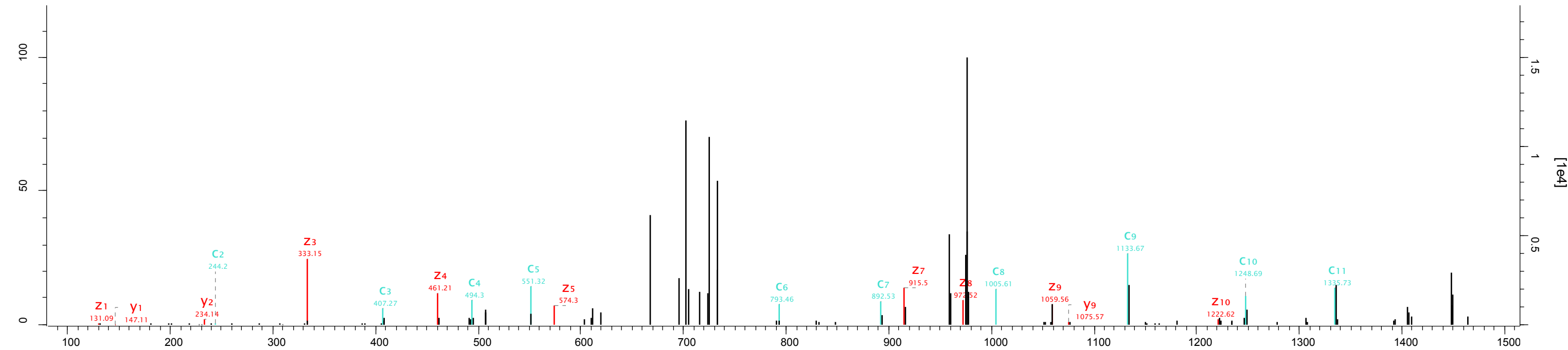
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

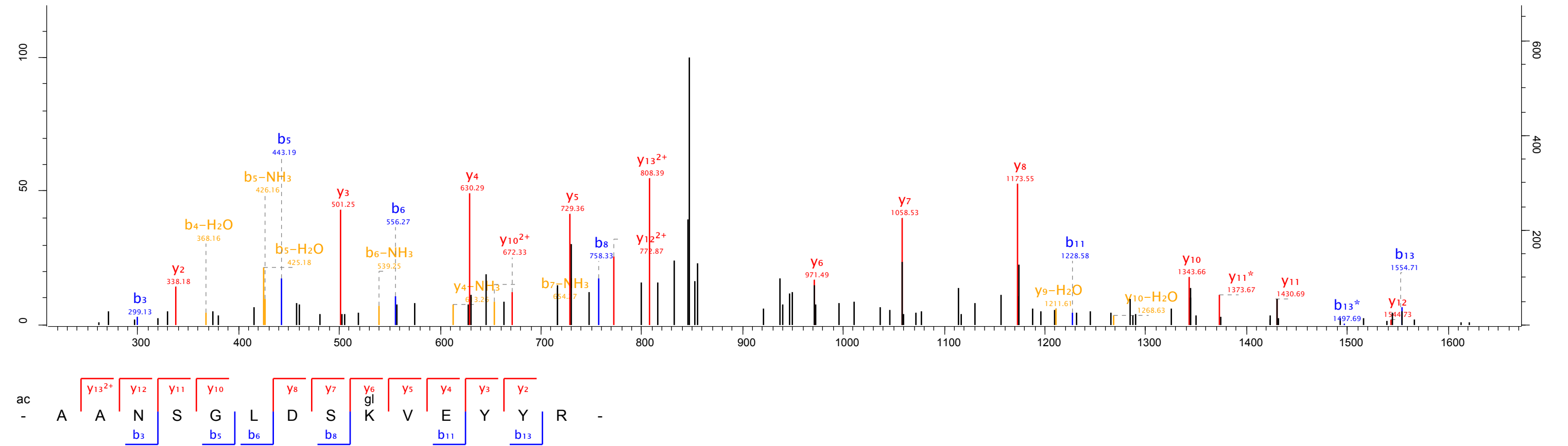
Scan	Method	Score	m/z
7052	ITMS; ETD	163.15	489.59

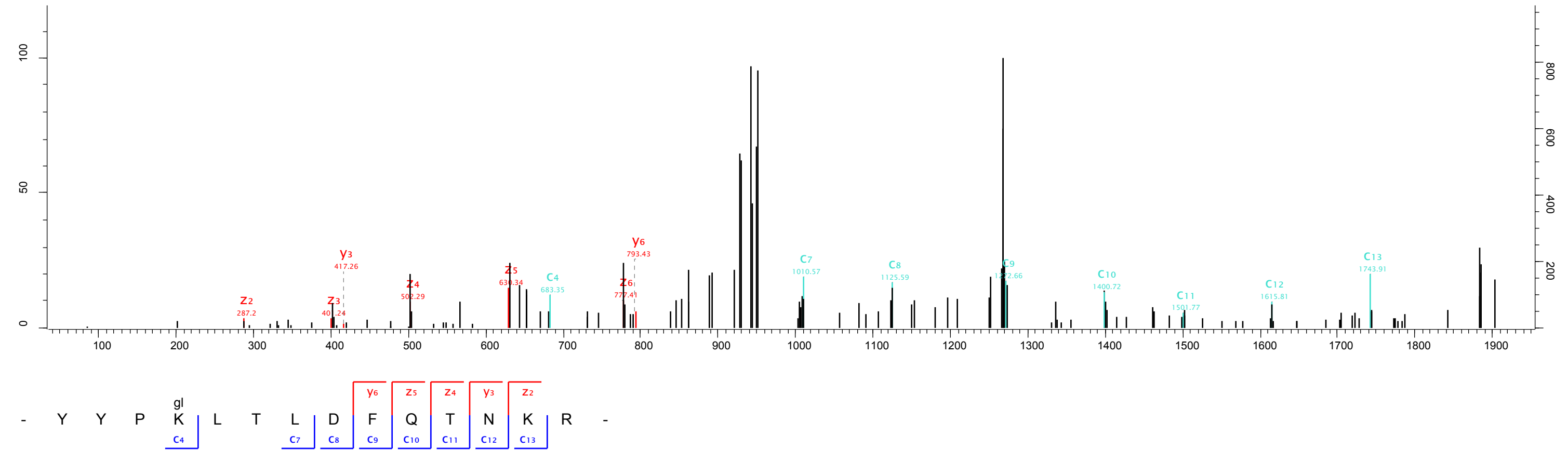


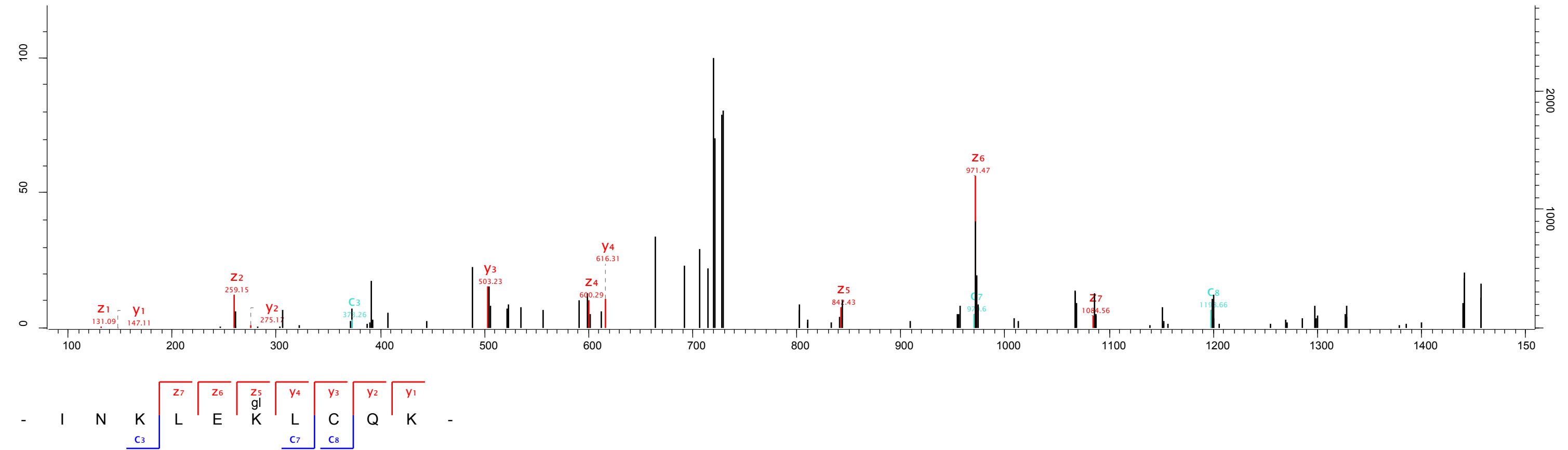
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_A_06August14_02

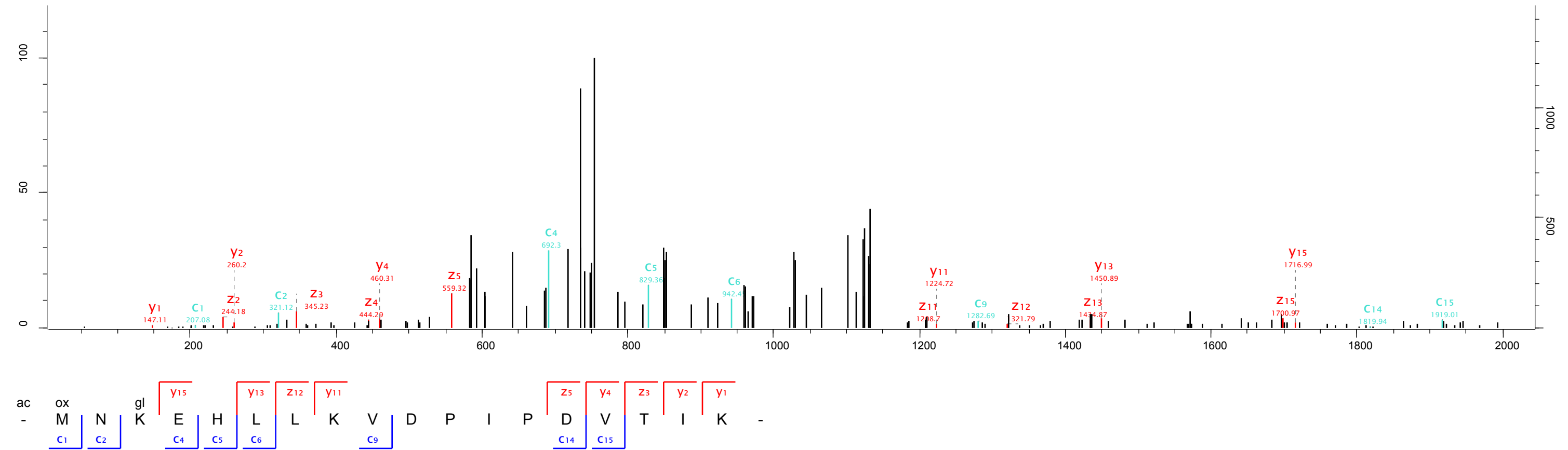
Scan	Method	Score	m/z
8620	ITMS; ETD	243.91	488.94





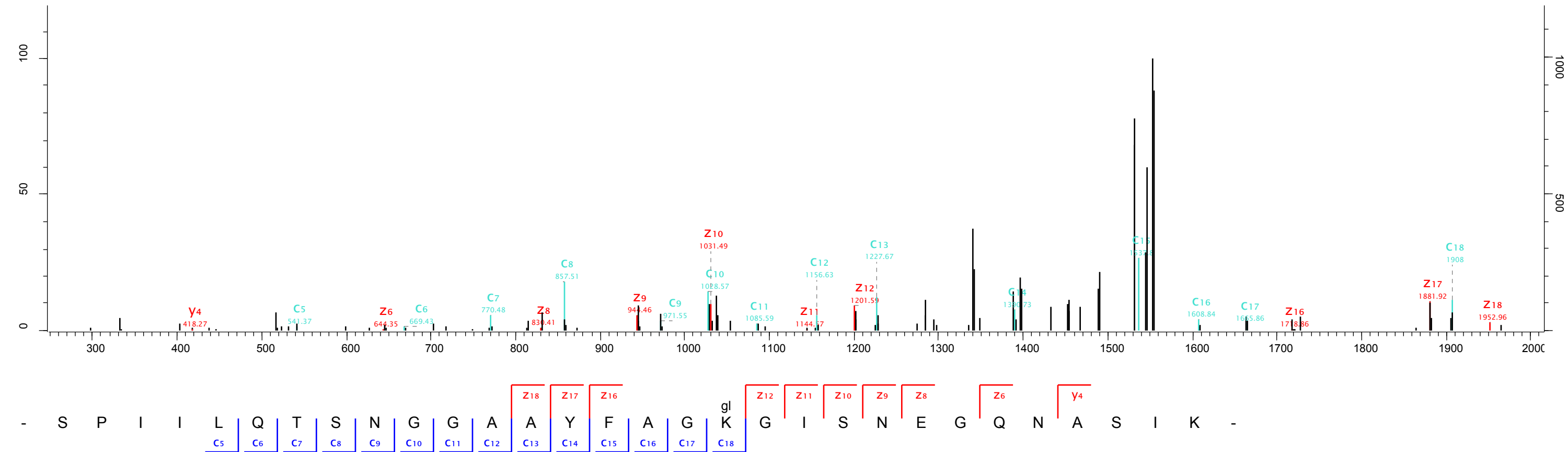






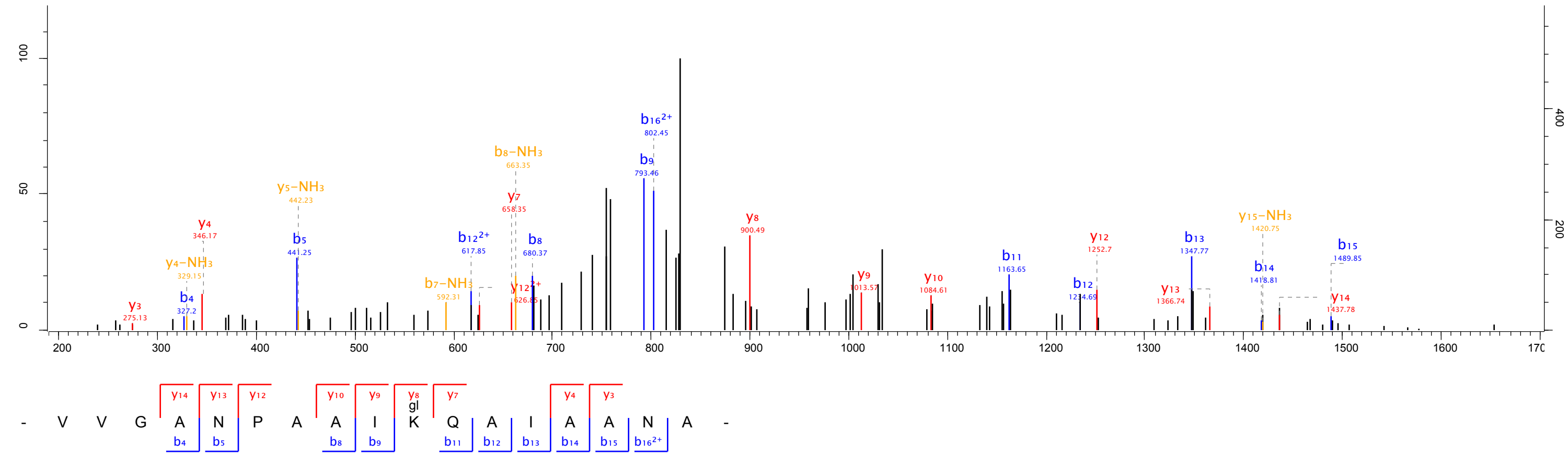
Raw file
tay_Yeast_Untreated_WCLip_GG-DDDT_B_06August14_06

Scan	Method	Score	m/z
17730	ITMS; ETD	165.01	1037.2



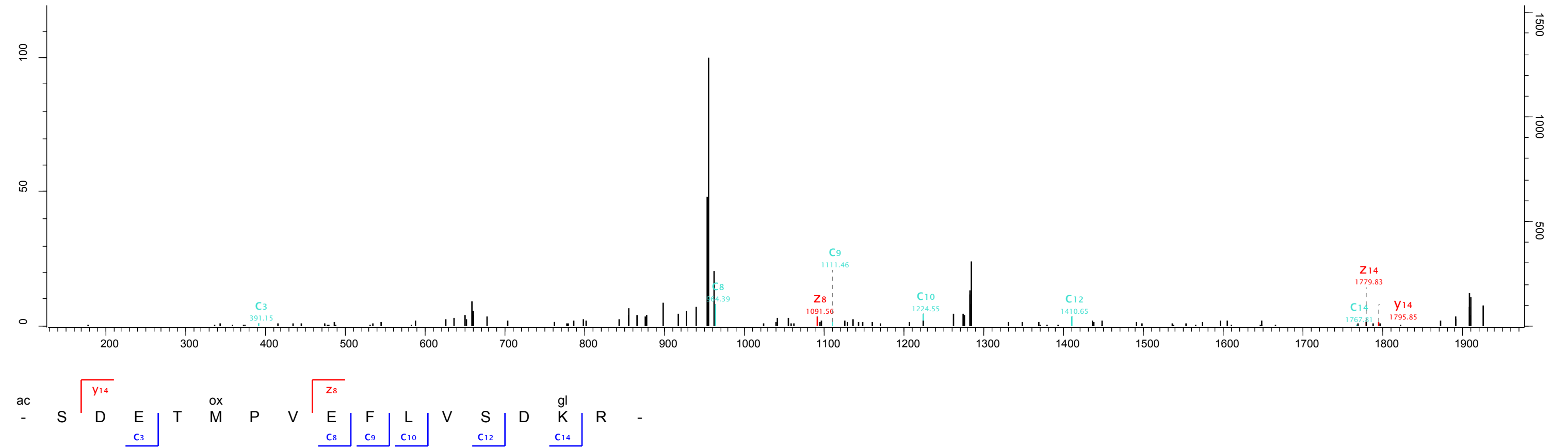
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_B_06August14_06

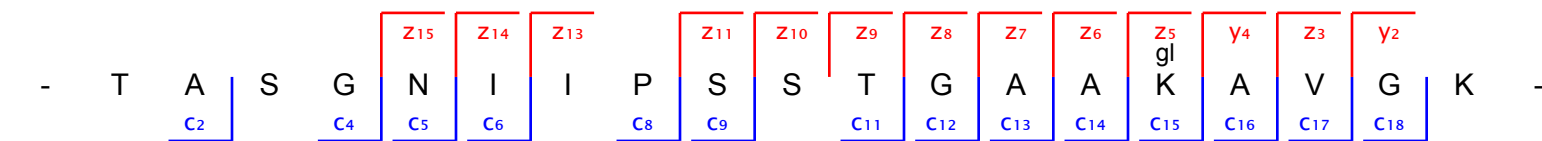
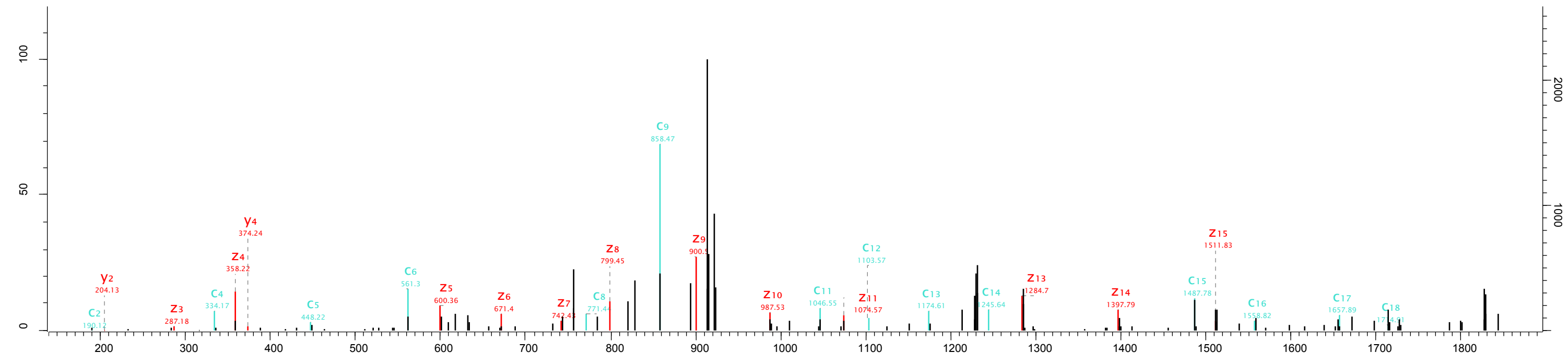
Scan	Method	Score	m/z
18672	ITMS; CID	108.36	847.47



Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_B_06August14_06

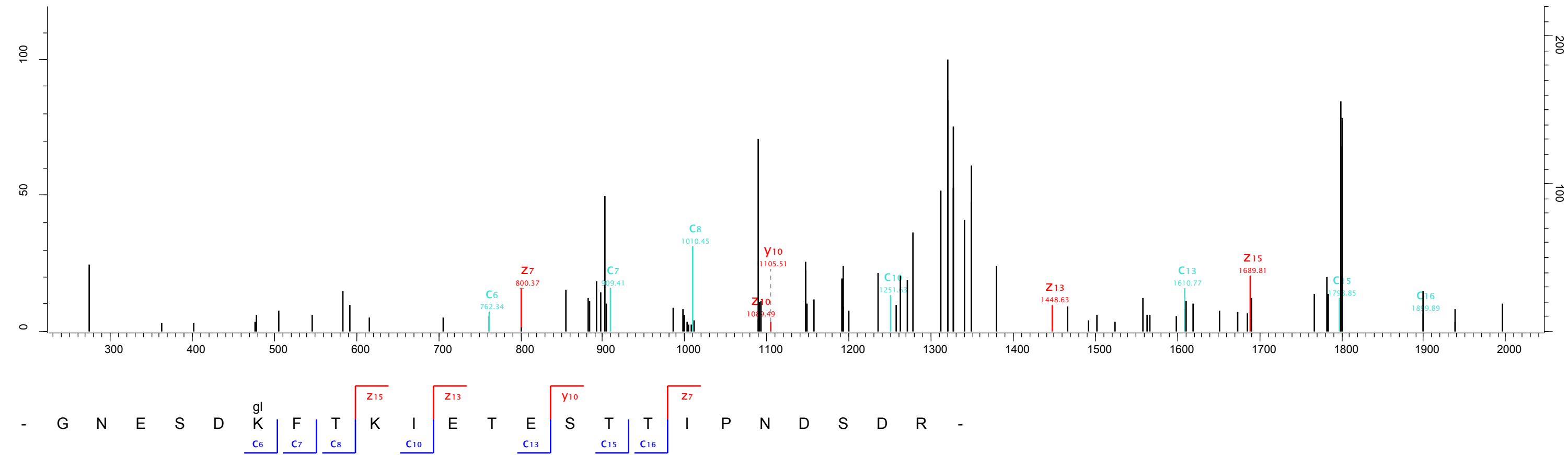
Scan	Method	Score	m/z
23331	ITMS; ETD	53.24	642.3

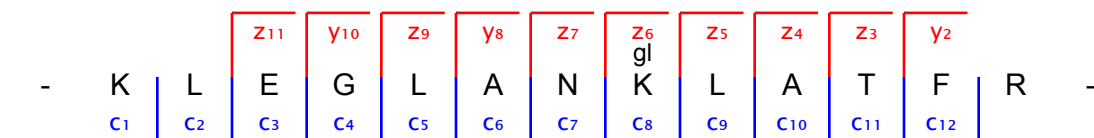
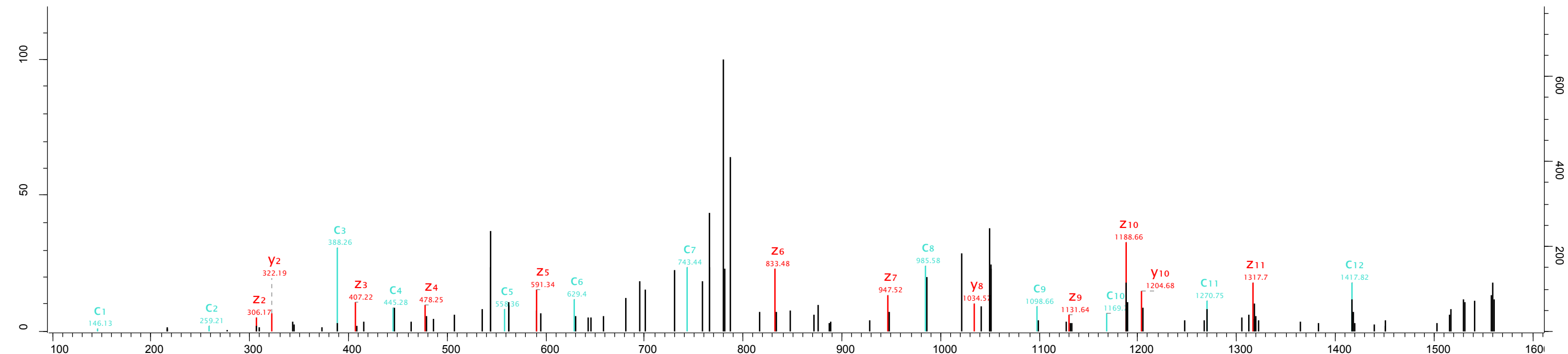




tay_Yeast_Untreated_WCLip_GG-DDDT_C_06August14_10

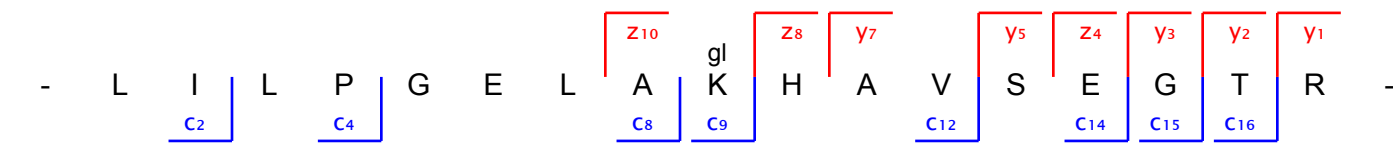
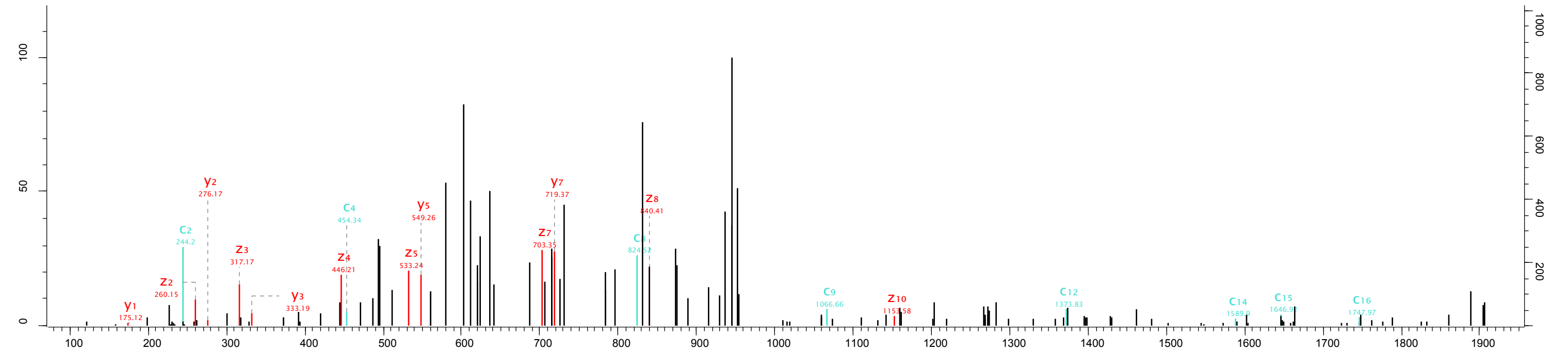
Scan	Method	Score	m/z
11770	ITMS; ETD	81.7	900.75





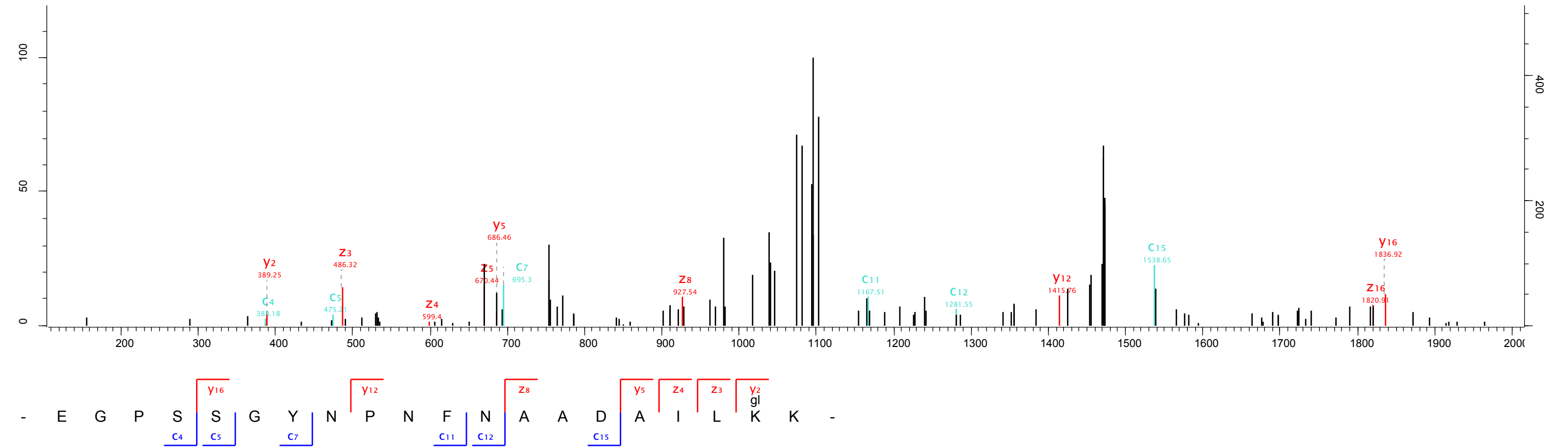
Raw file
tay_Yeast_Untreated_WCLip_GG-DDDT_C_06August14_10

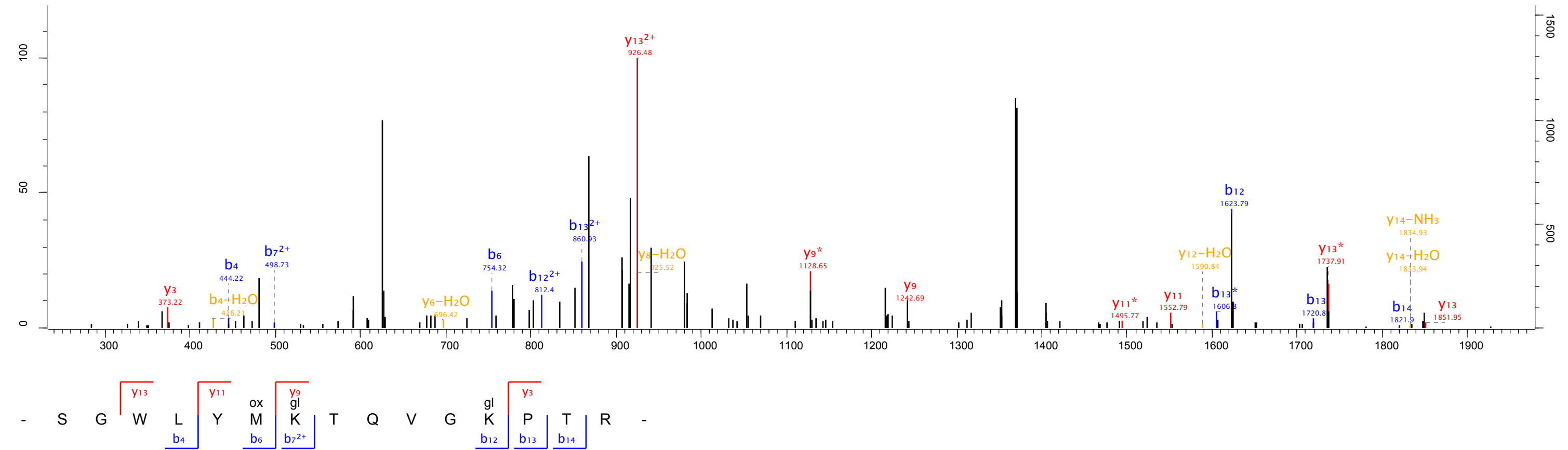
Scan	Method	Score	m/z
15262	ITMS; ETD	171.29	477.02

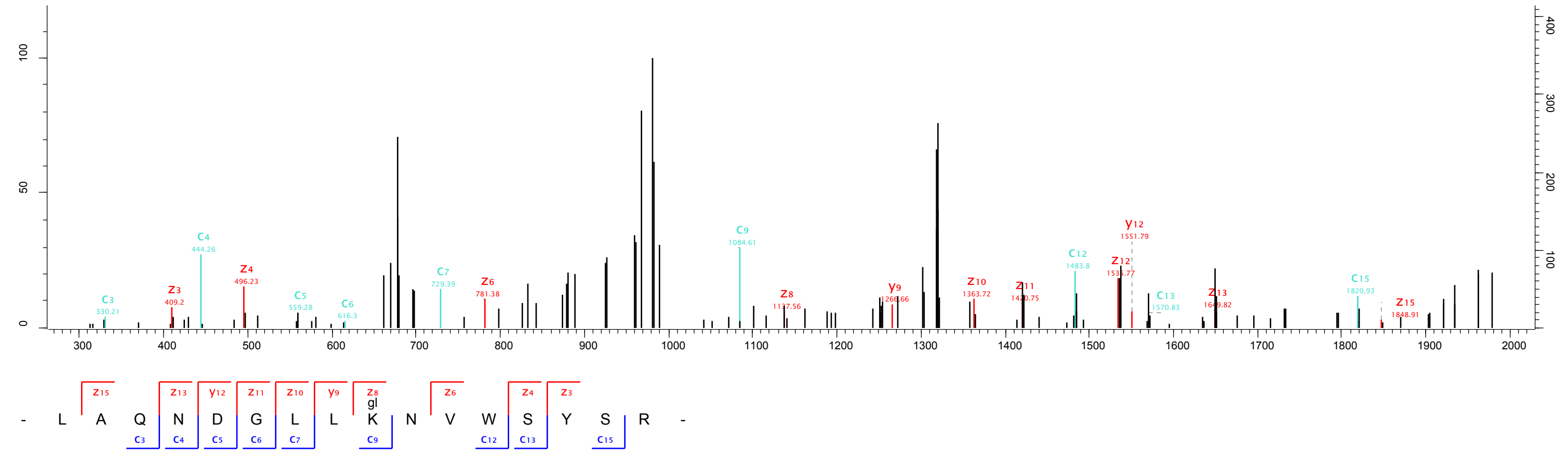


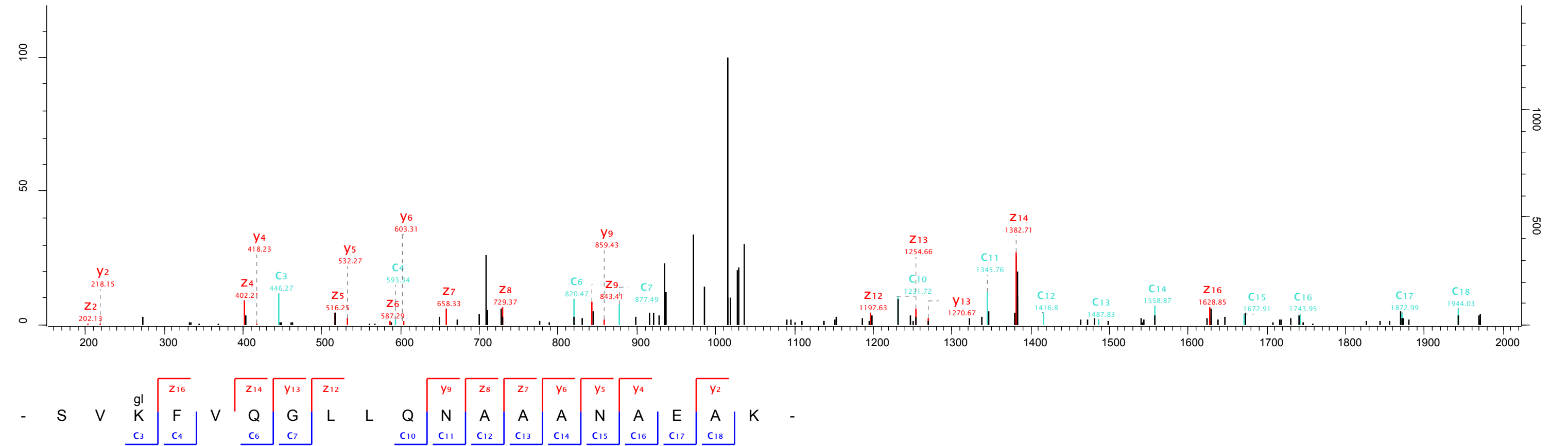
tay_Yeast_Untreated_WCLip_GG-DDDT_C_06August14_10

Scan	Method	Score	m/z
15734	ITMS; ETD	83.95	736.7



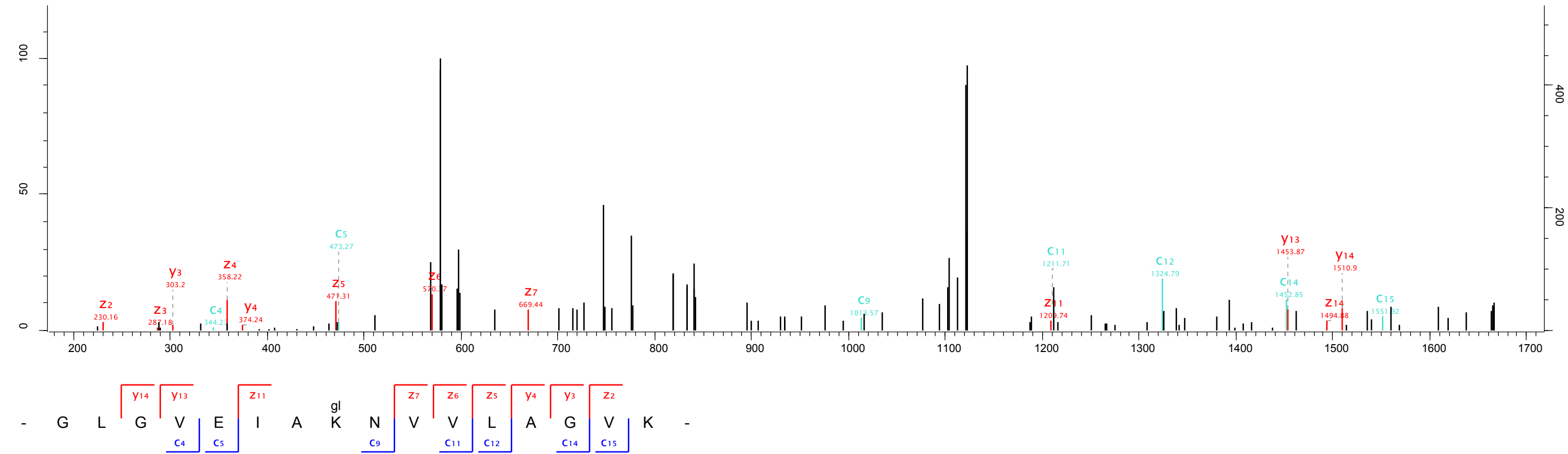






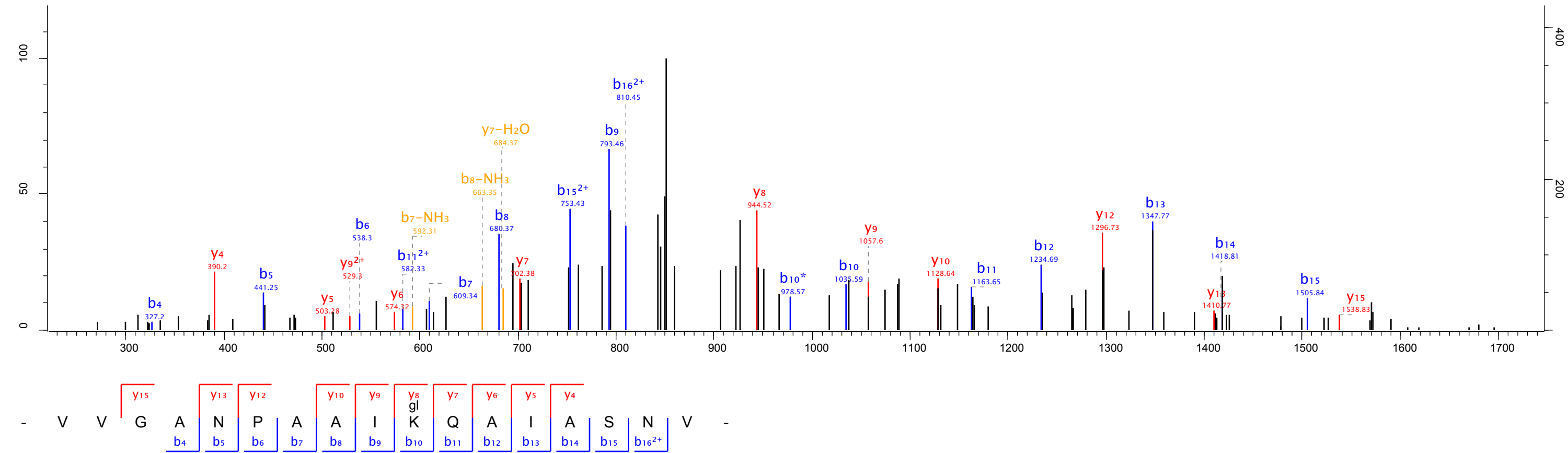
Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_C_06August14_10

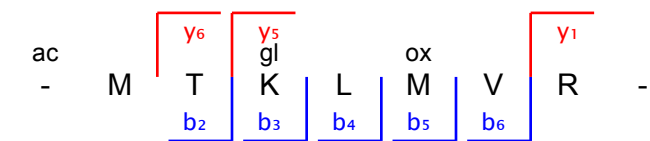
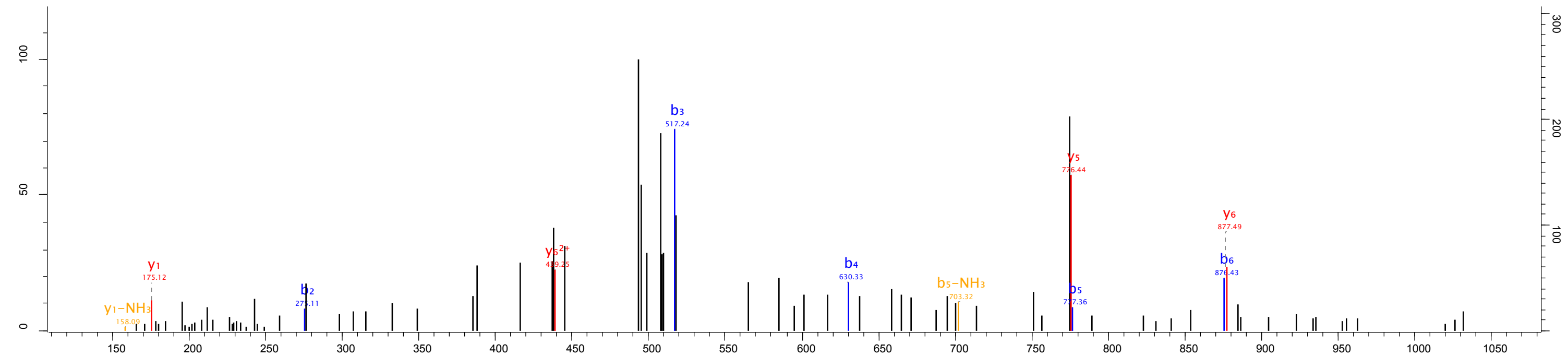
Scan	Method	Score	m/z
20599	ITMS; ETD	95.18	561.34

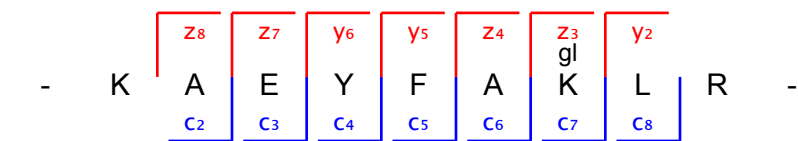
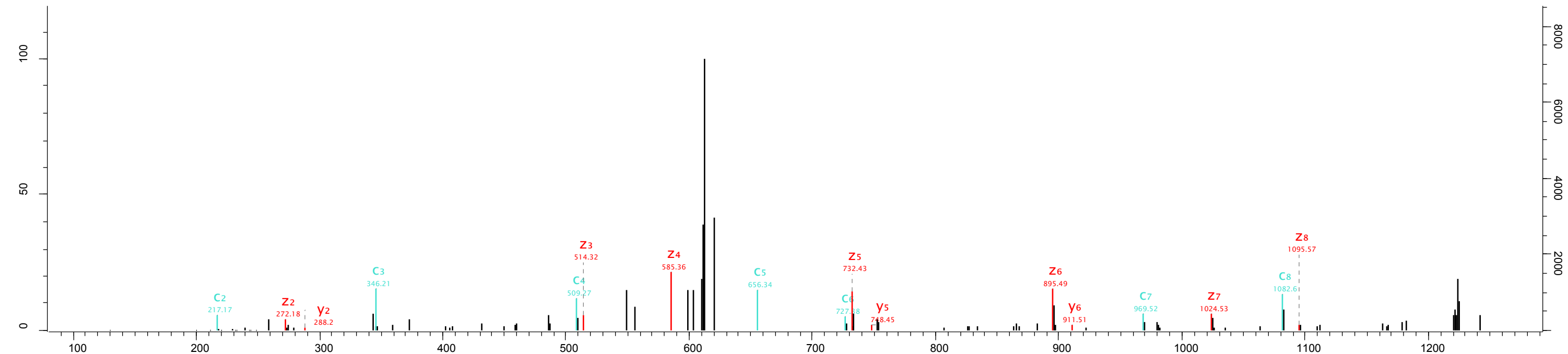


Raw file
tay_Yeast_Untreated_WCLip_GG_DDDT_C_06August14_10

Scan	Method	Score	m/z
20954	ITMS; CID	109.67	869.49

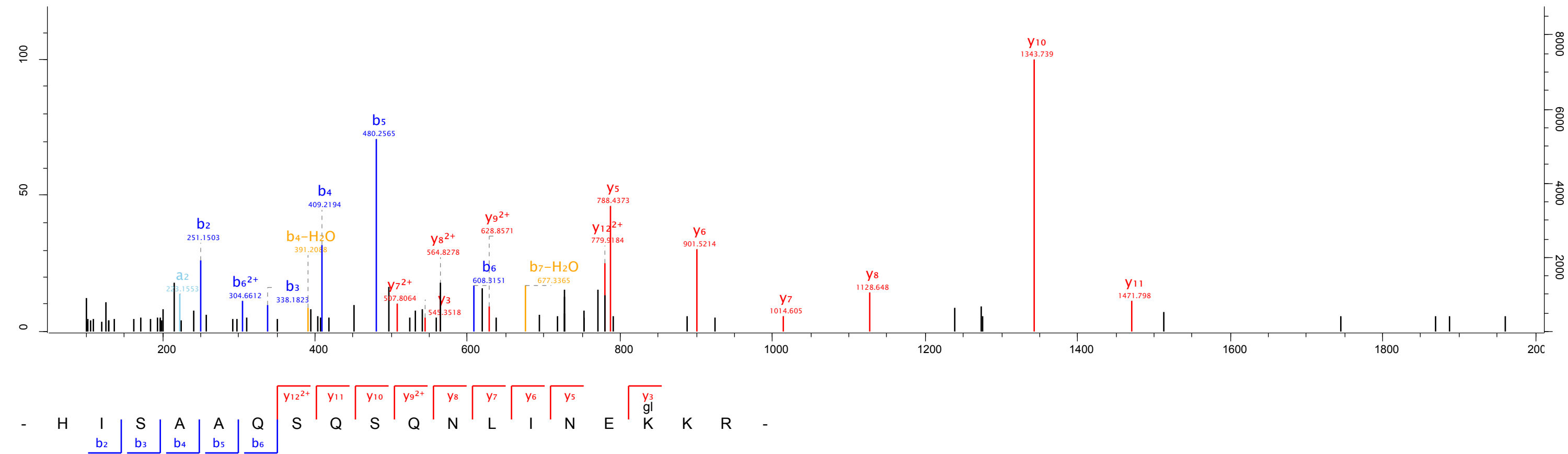


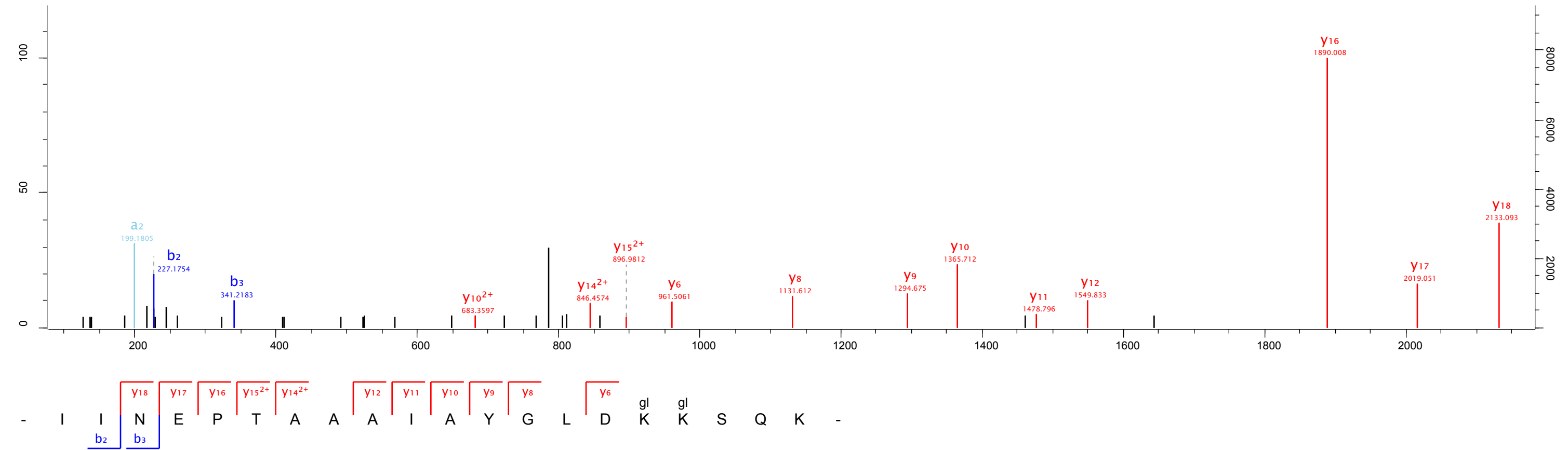


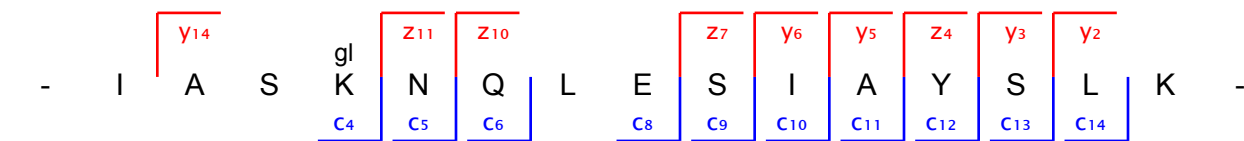
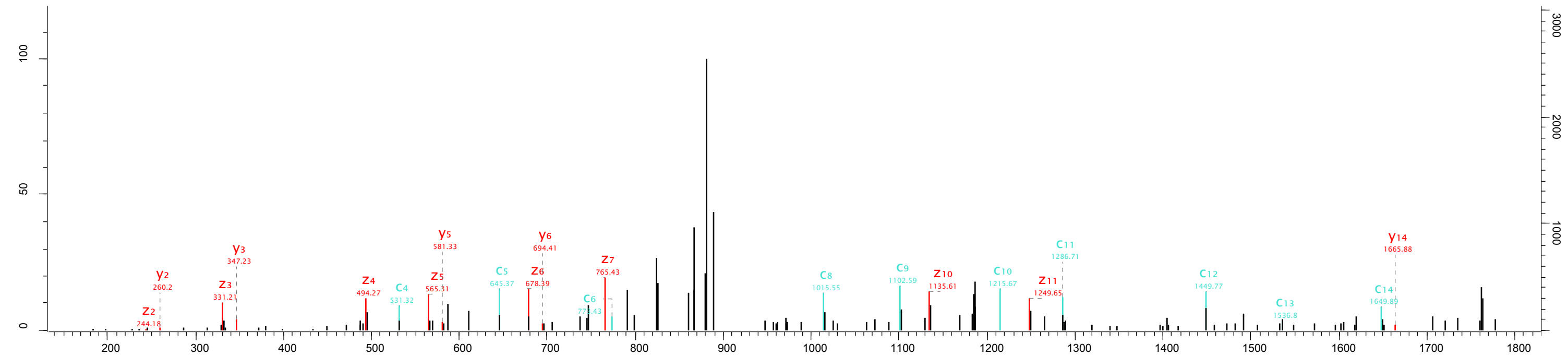


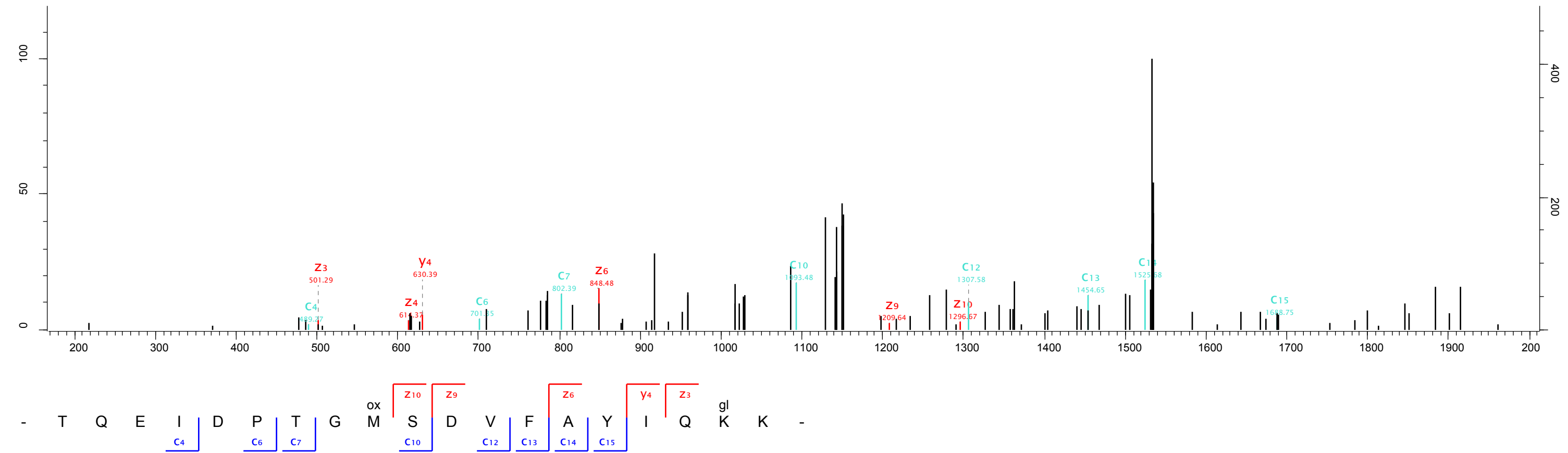
Scan	Method	Score	m/z
------	--------	-------	-----

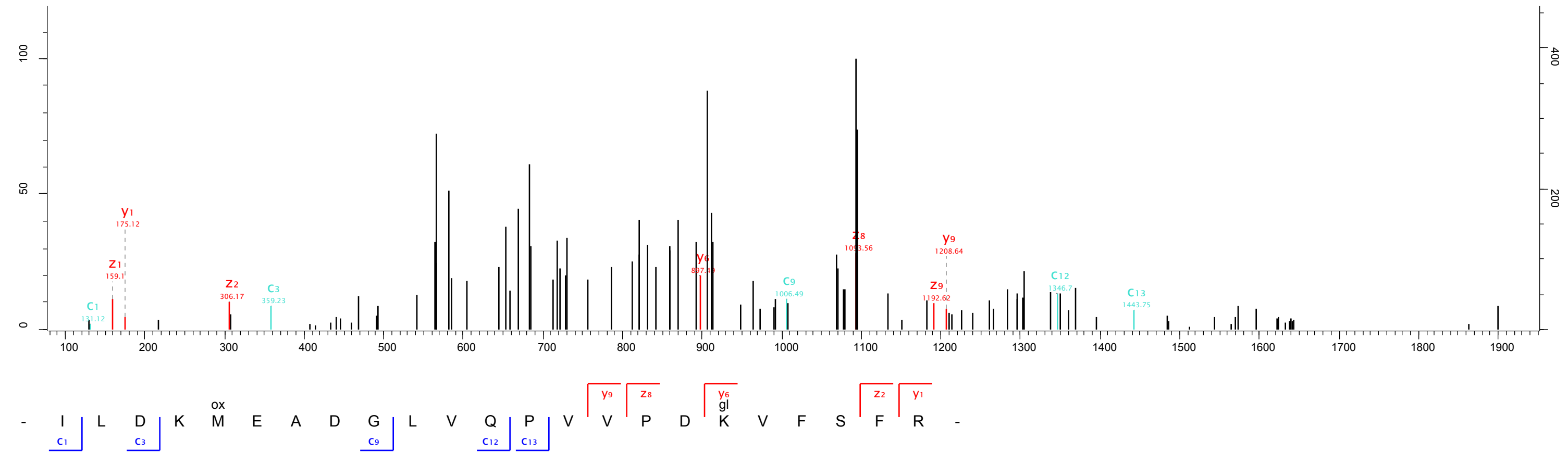
1234	FTMS; HCD	81.66	542.54
------	-----------	-------	--------

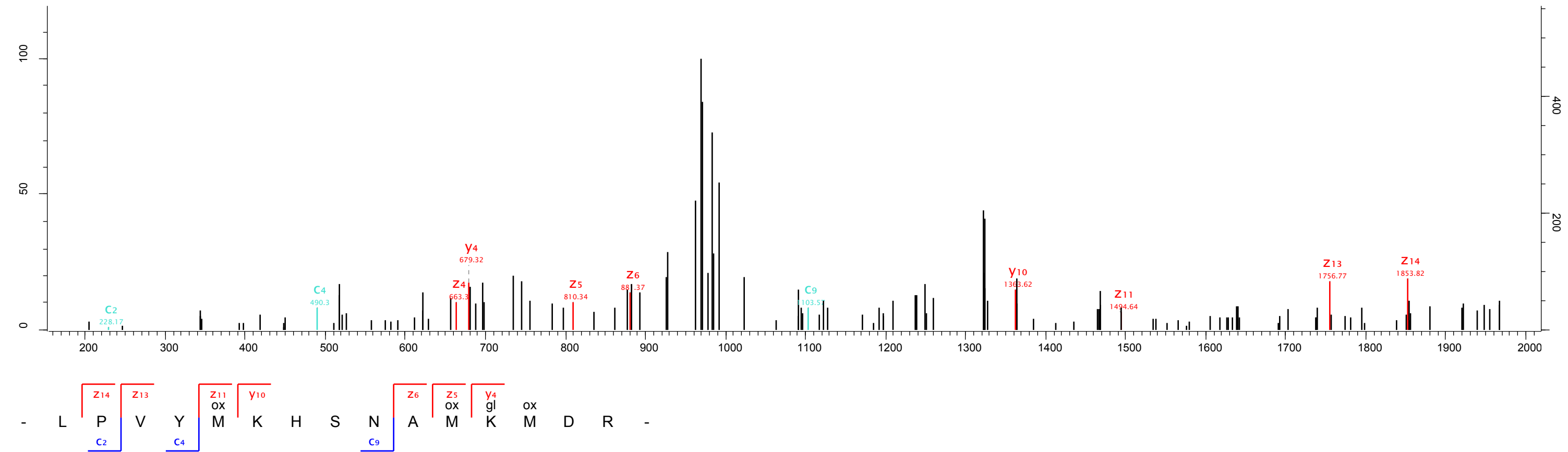


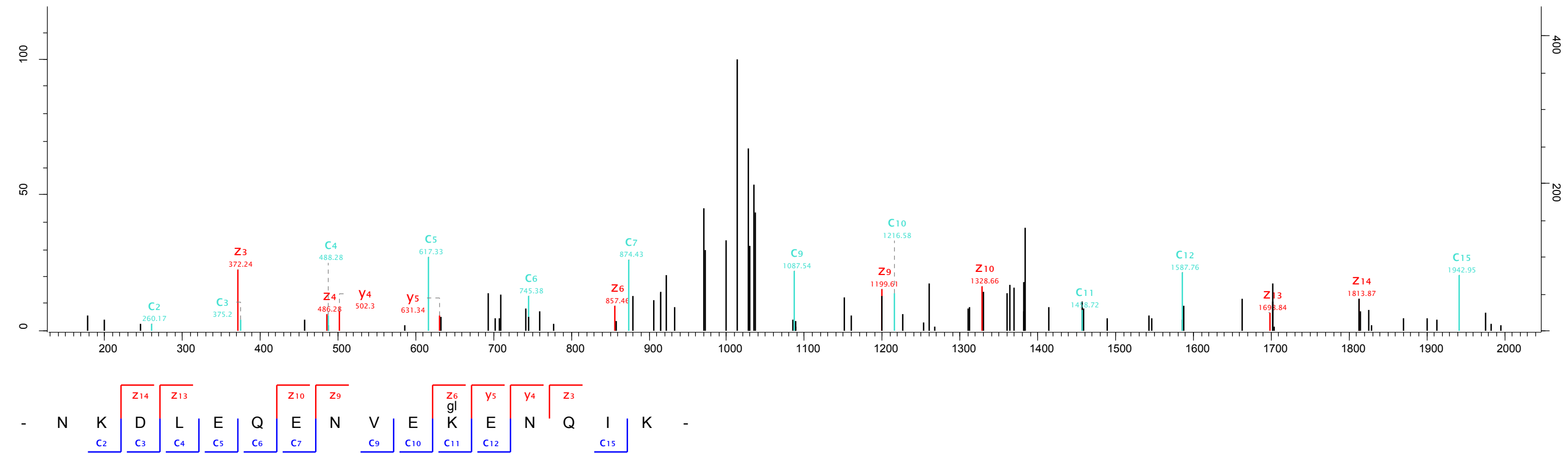


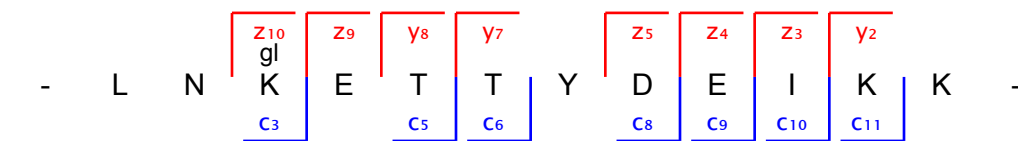
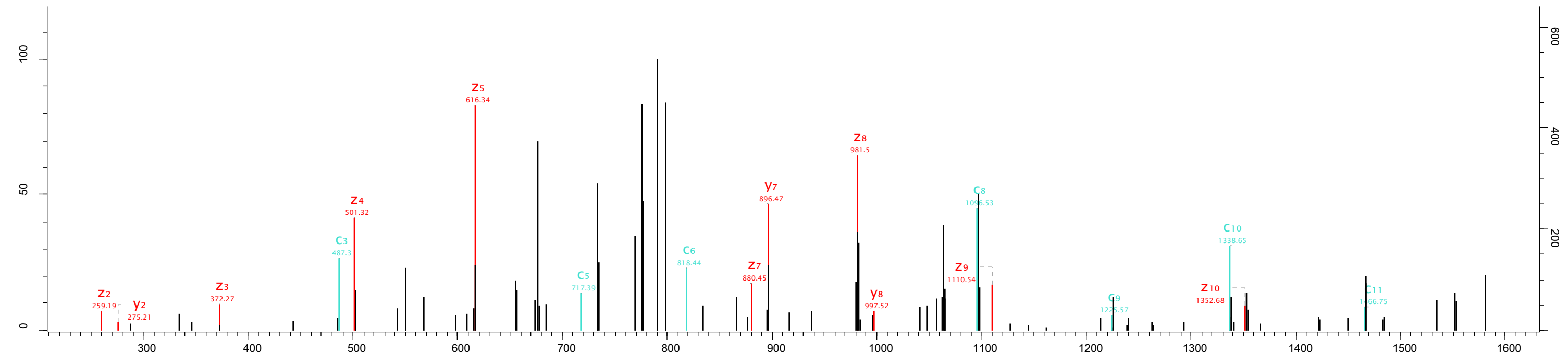


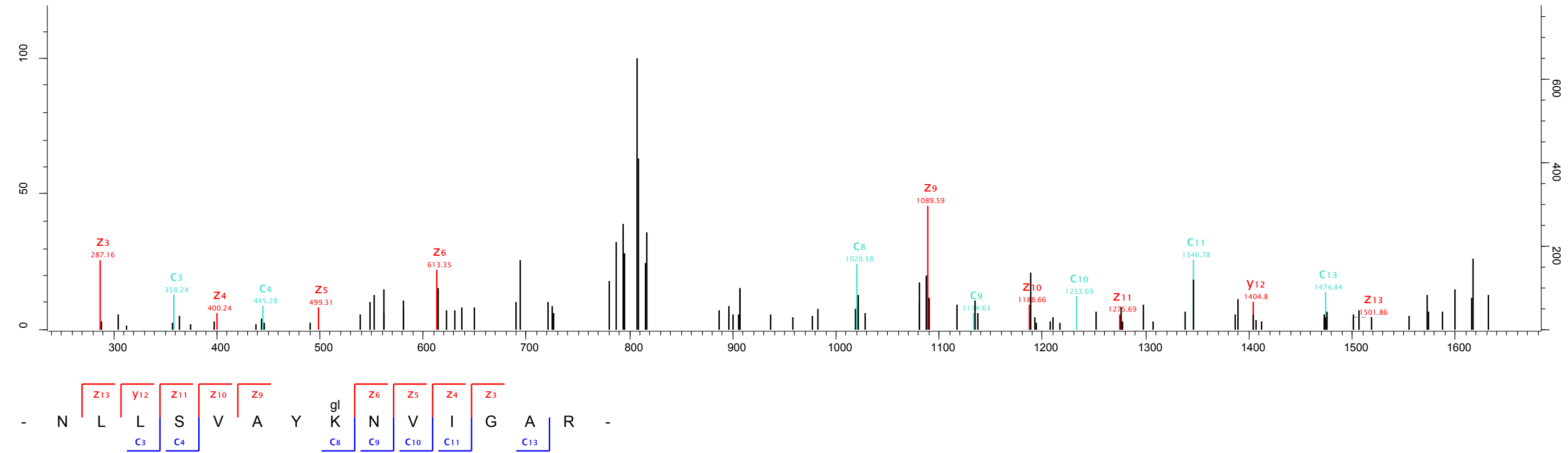


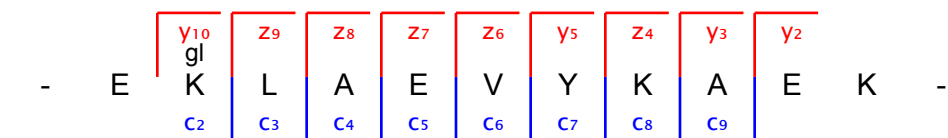
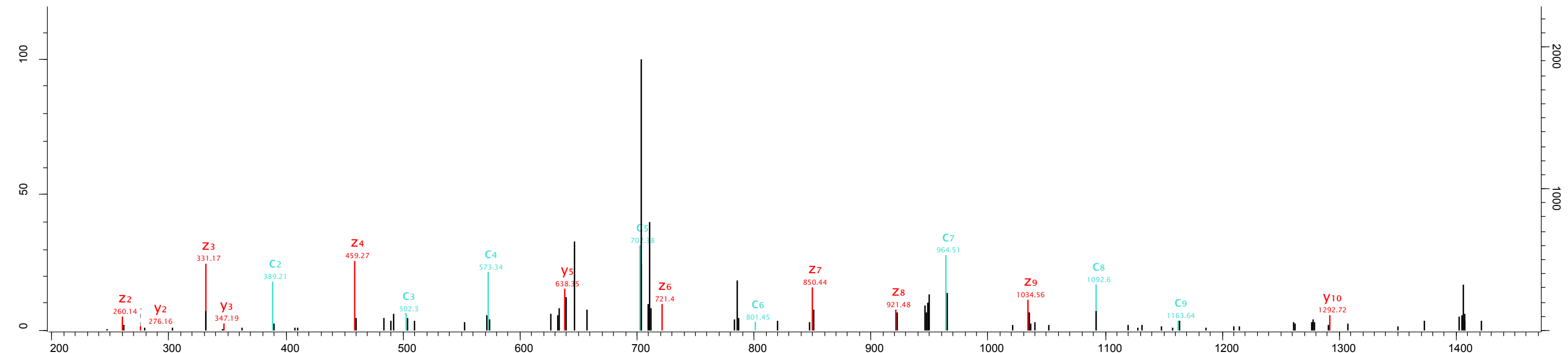


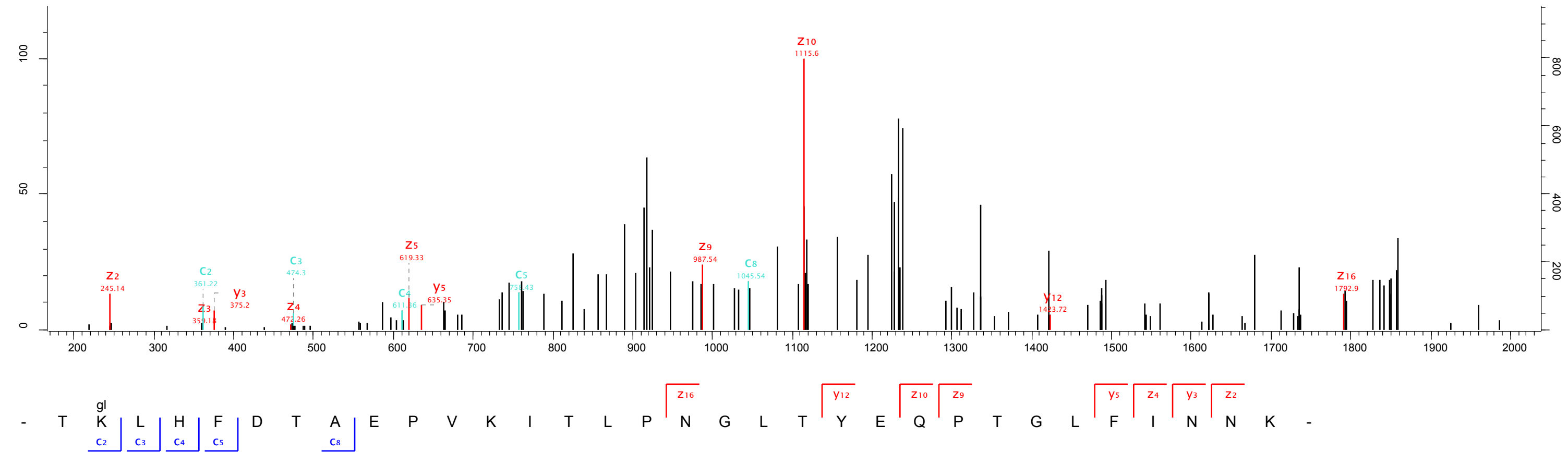


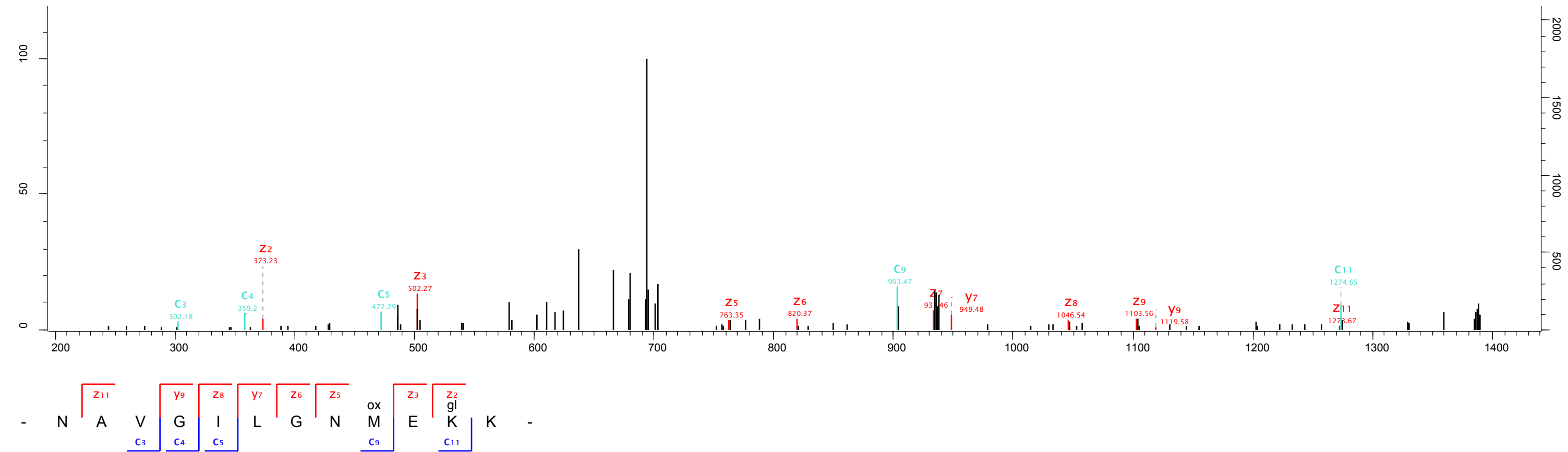


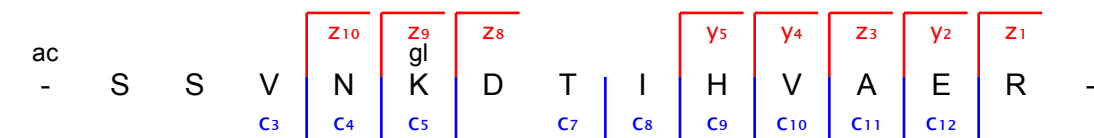
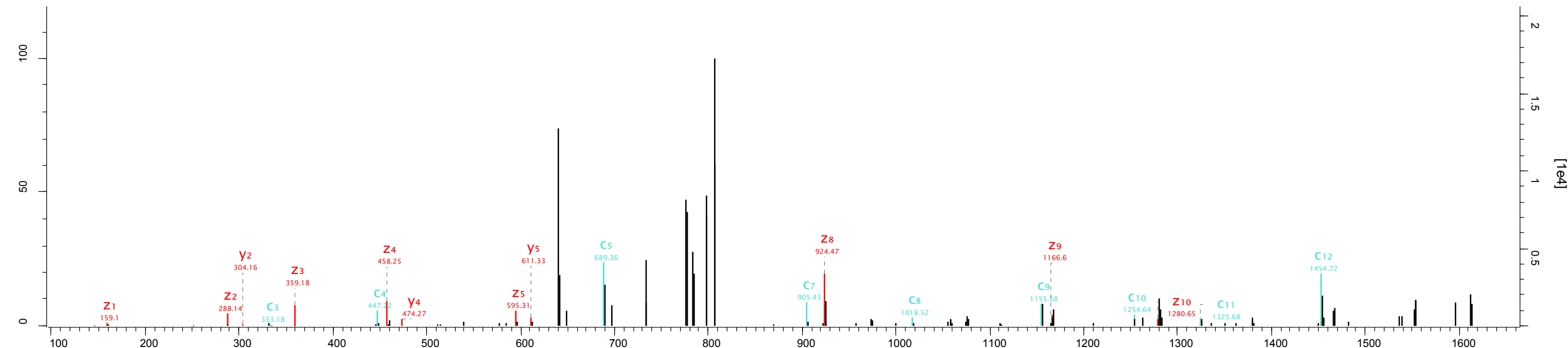


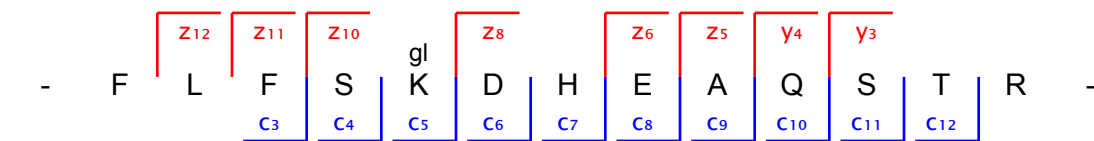
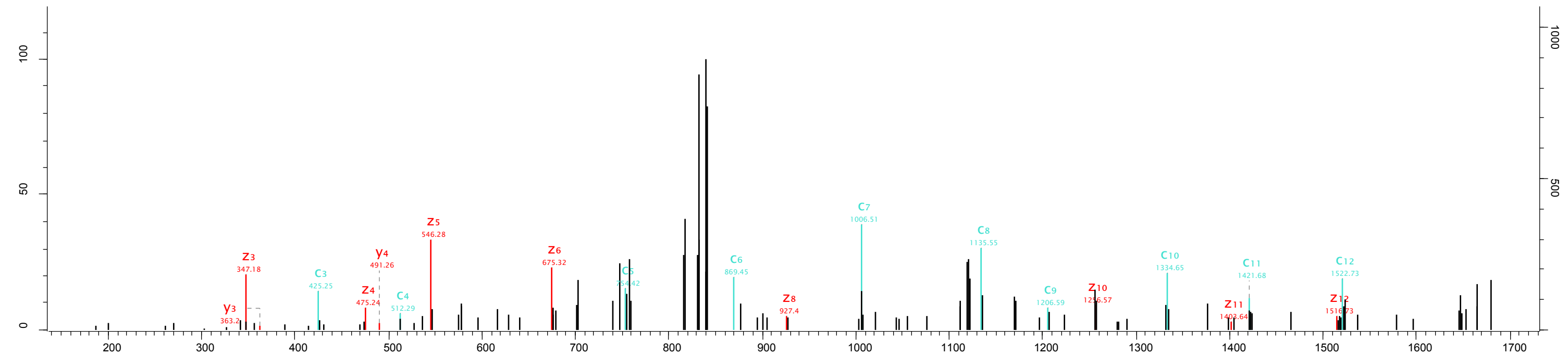


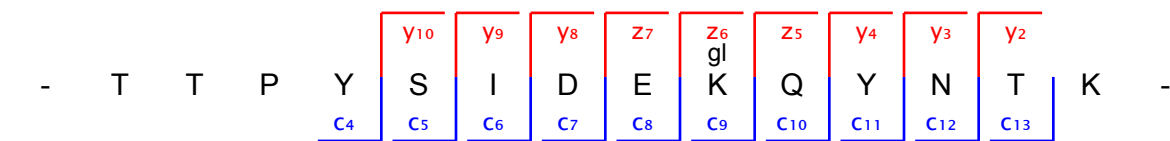
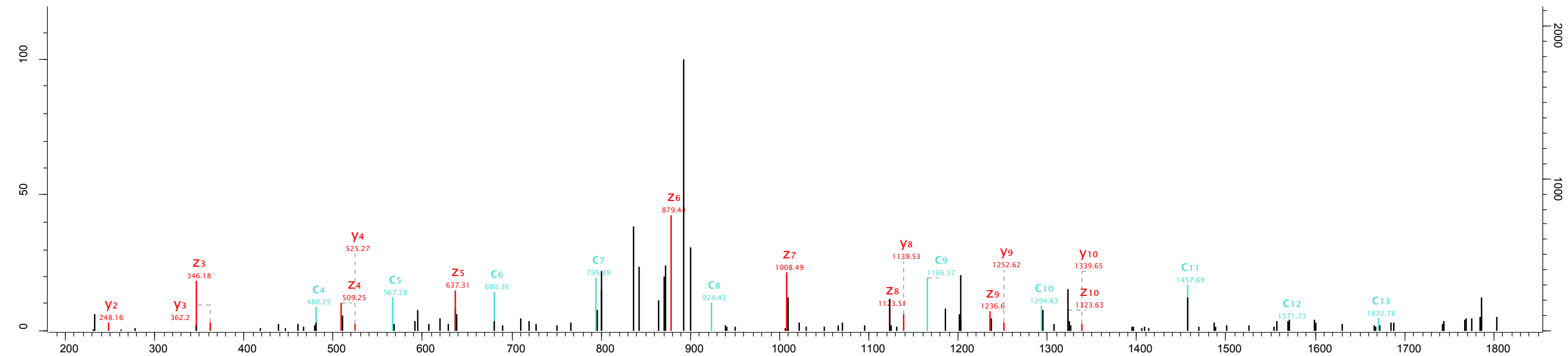






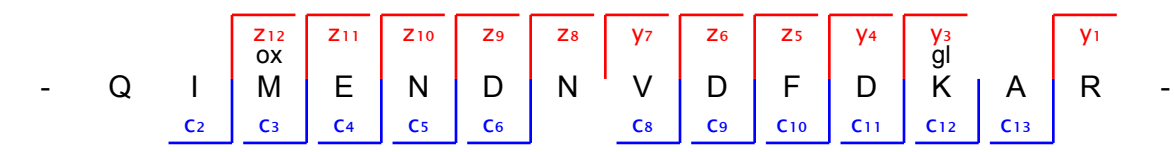
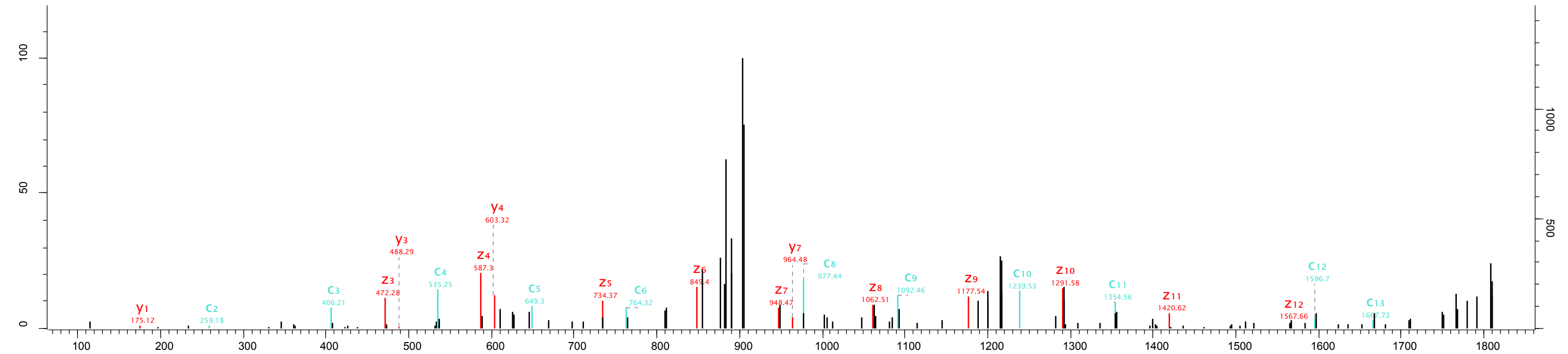


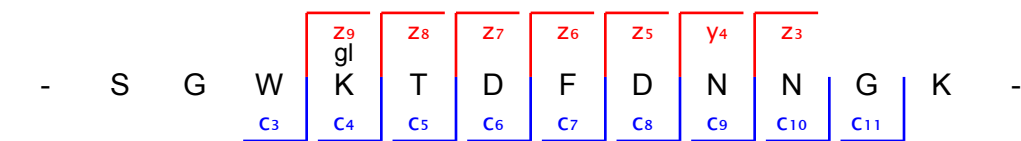
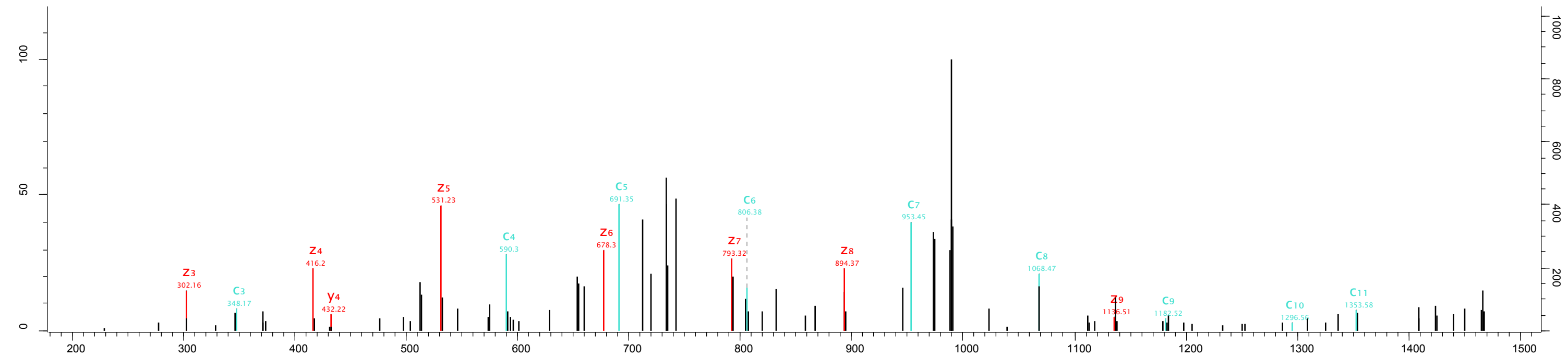


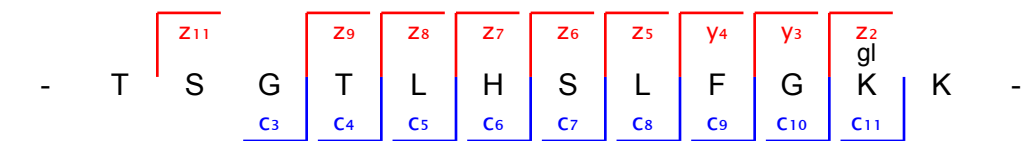
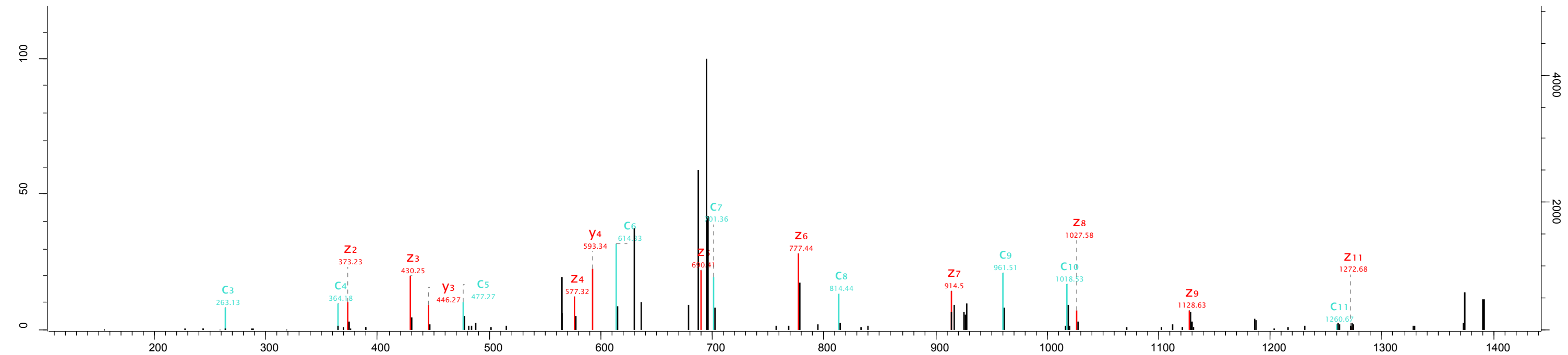


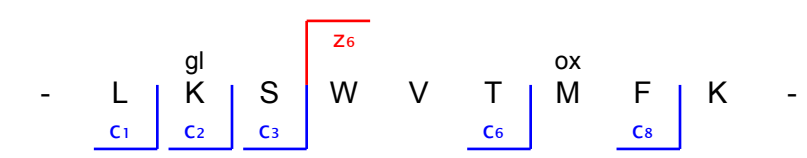
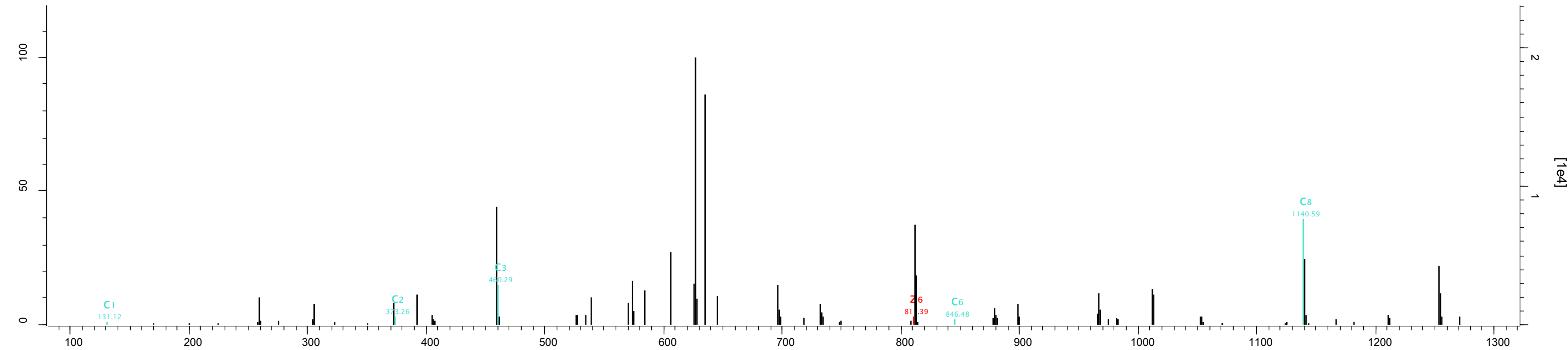
tay_Yeast_Untreated_WCLip_GG_plus3andUp_etd_01August14_02

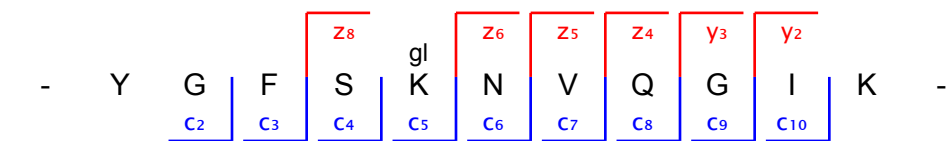
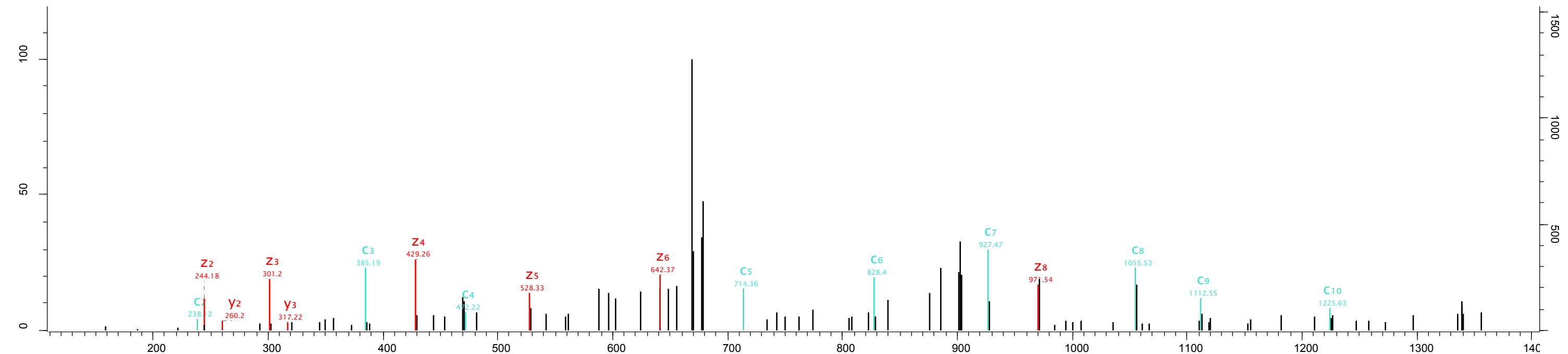
Scan	Method	Score	m/z
2542	ITMS; ETD	250.67	608.94

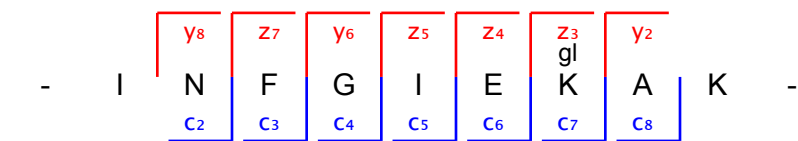
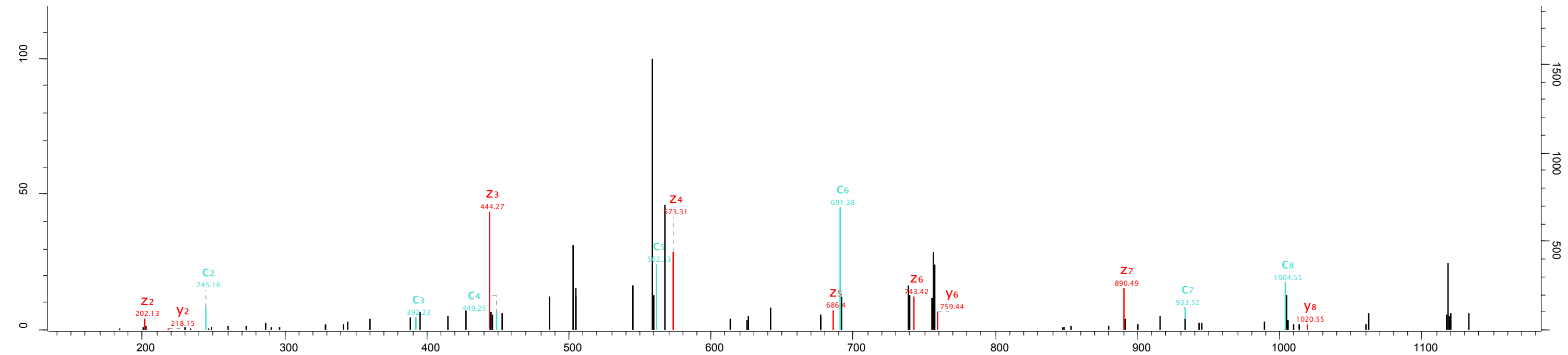


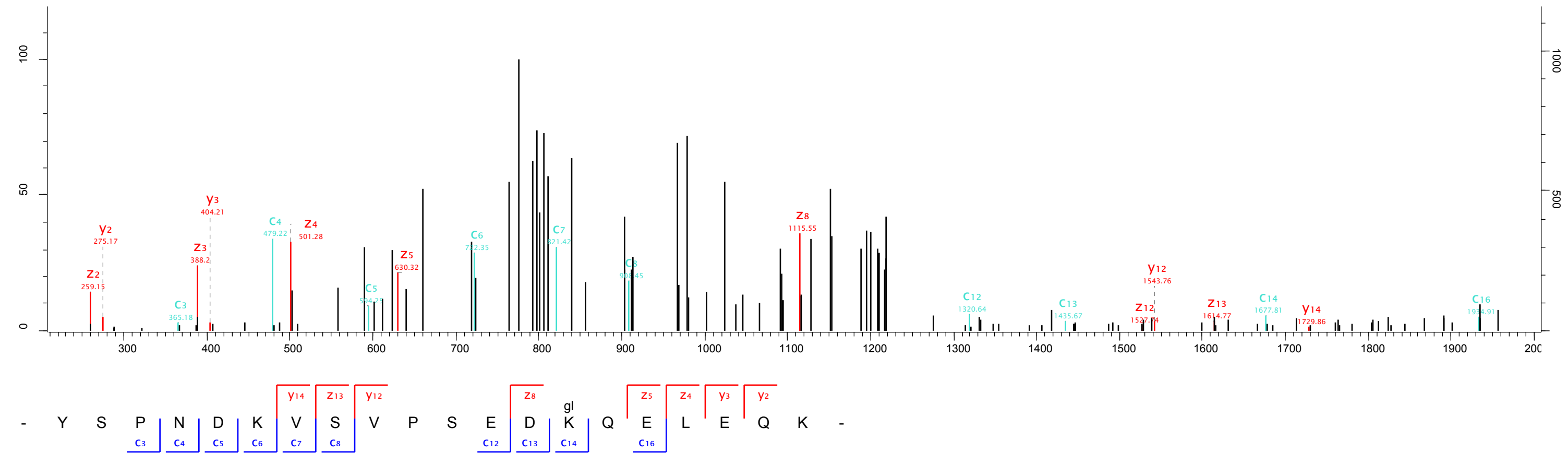


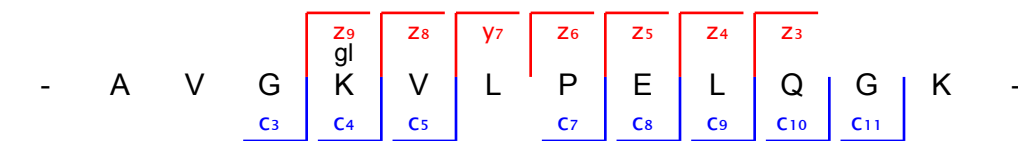
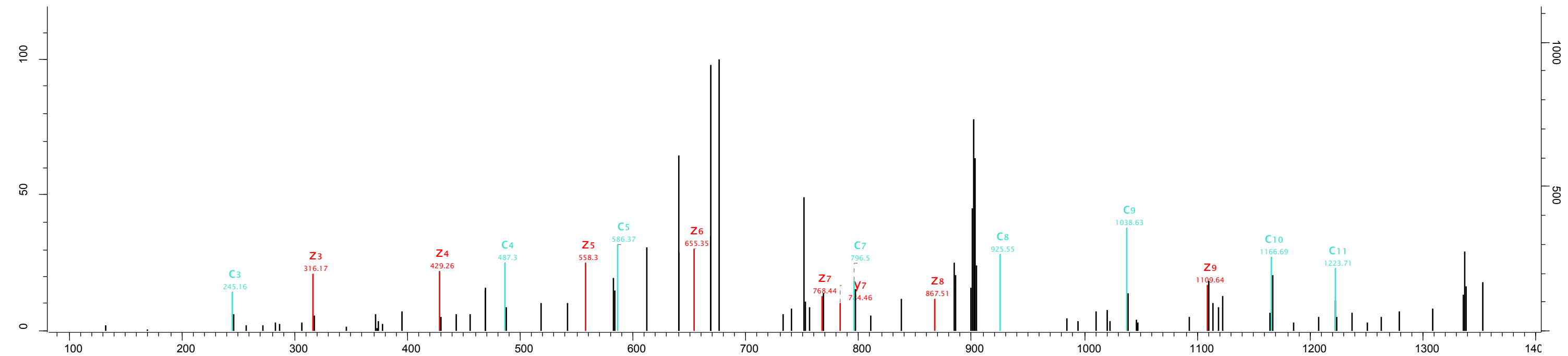


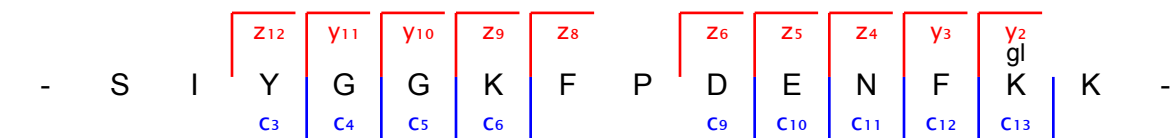
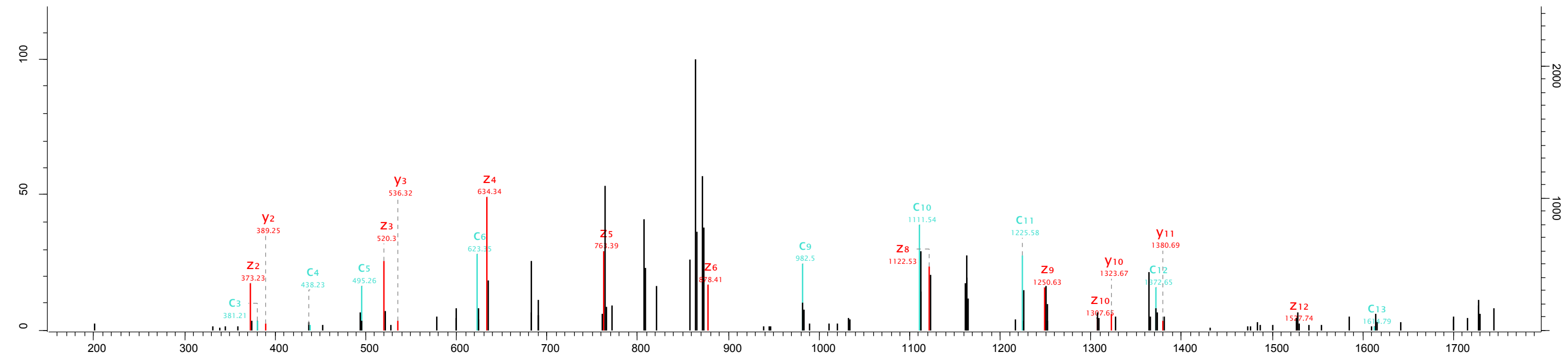


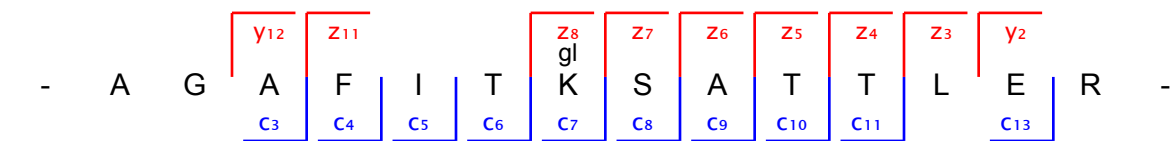
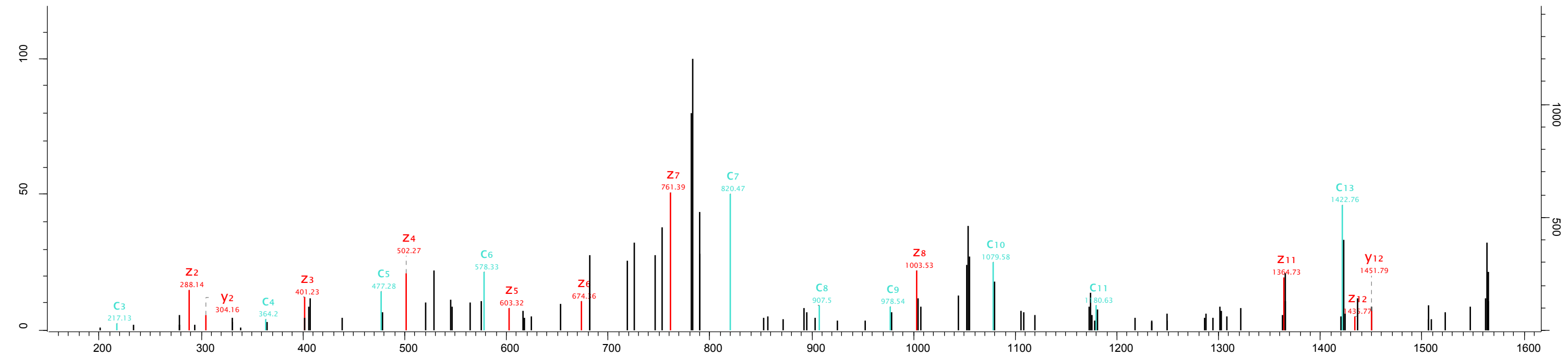






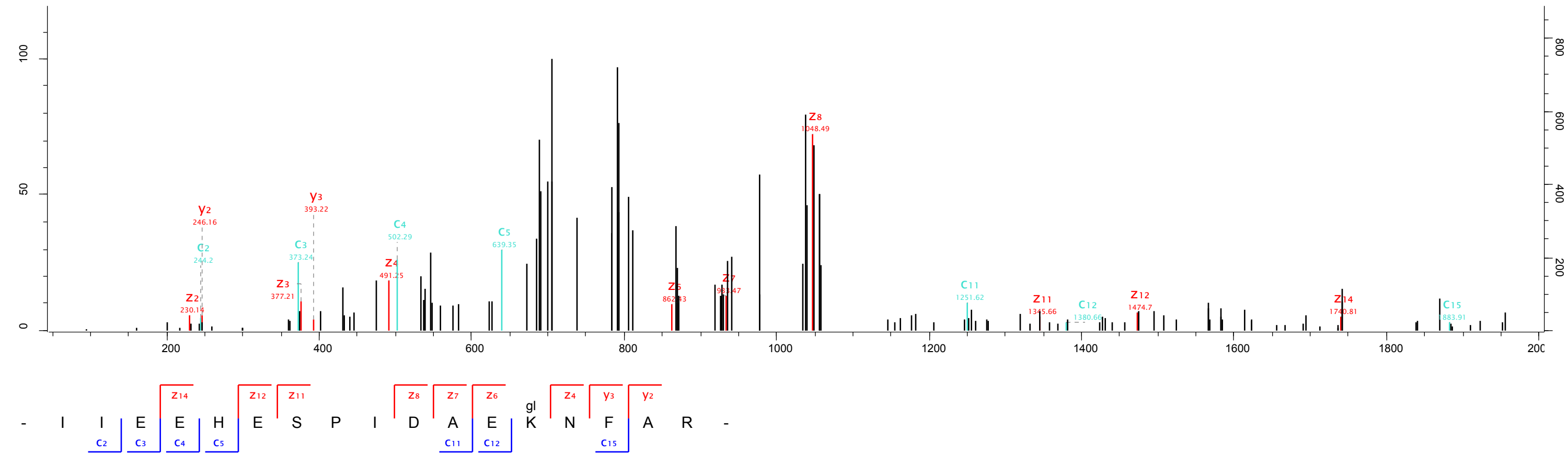


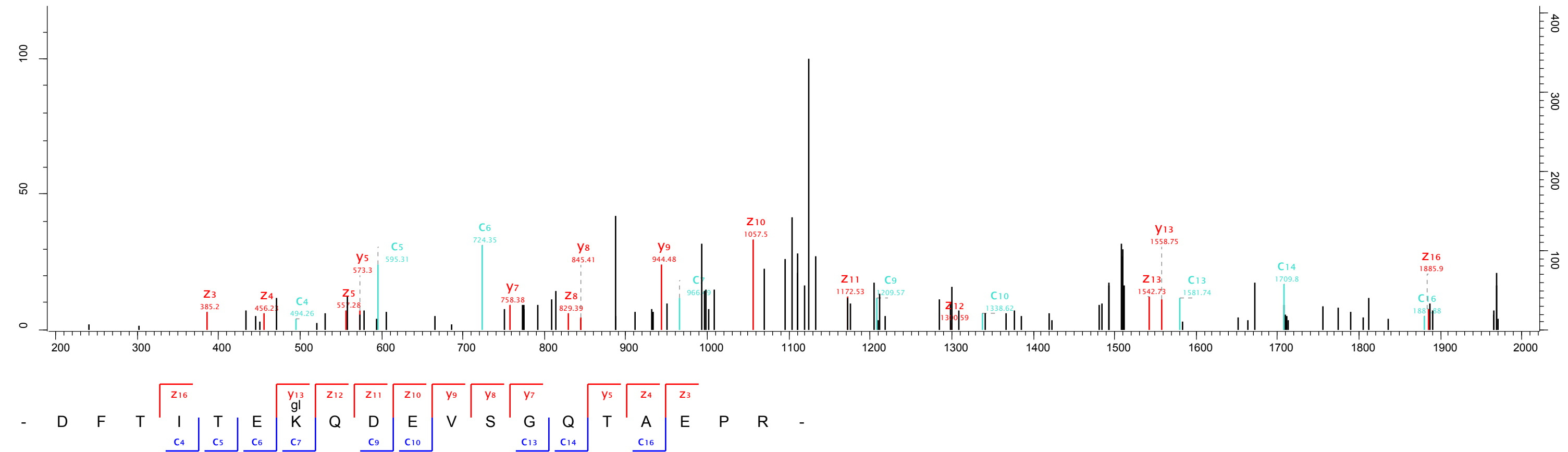


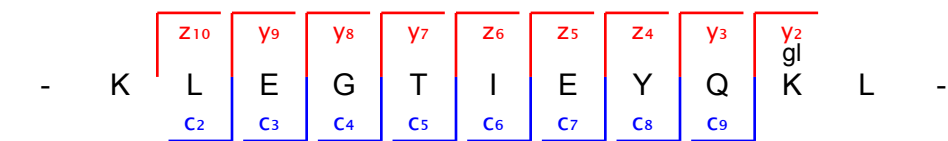
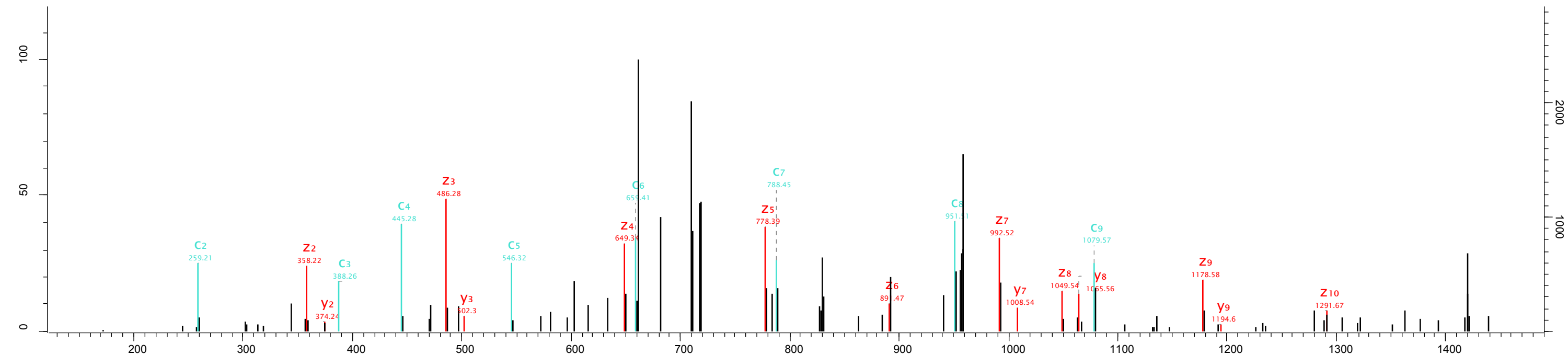


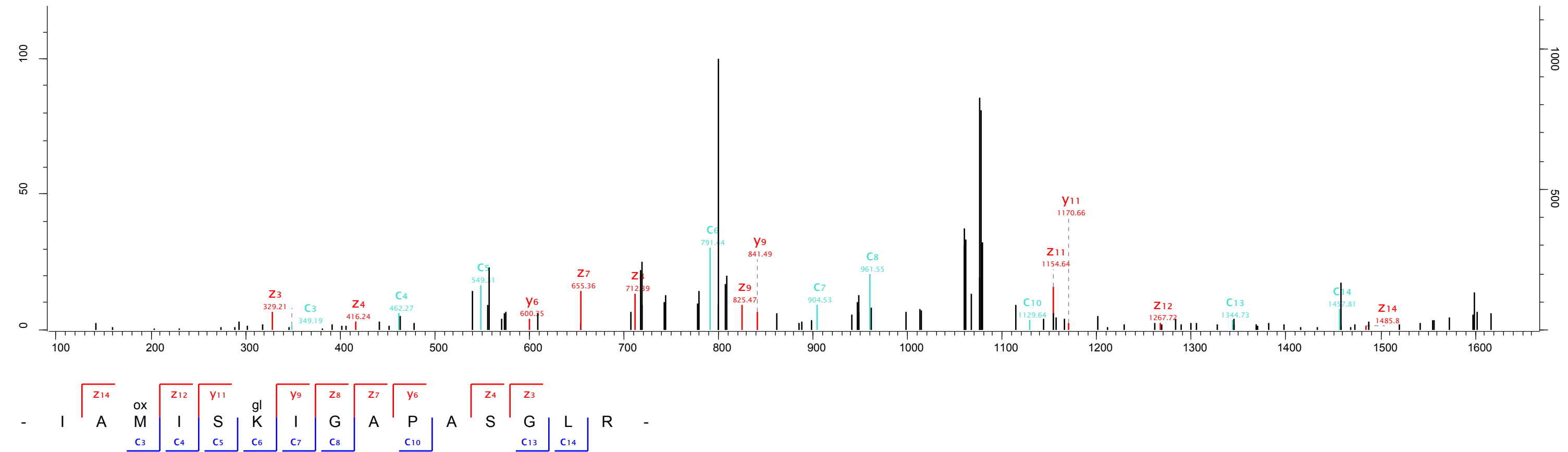
Scan	Method	Score	m/z
------	--------	-------	-----

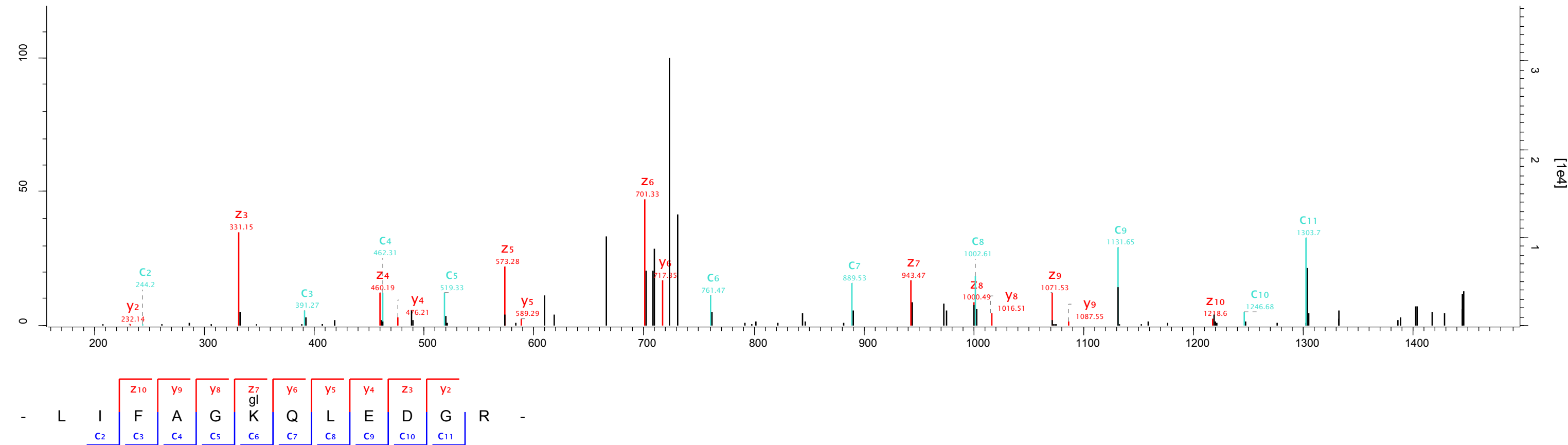
5167	ITMS; ETD	105.46	528.76
------	-----------	--------	--------

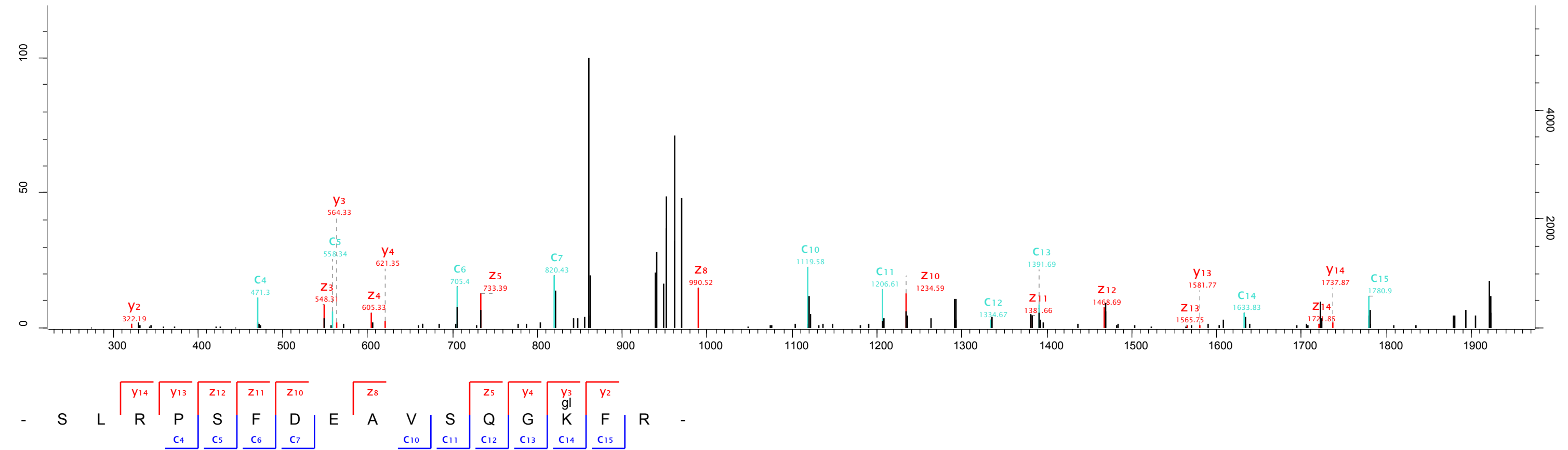


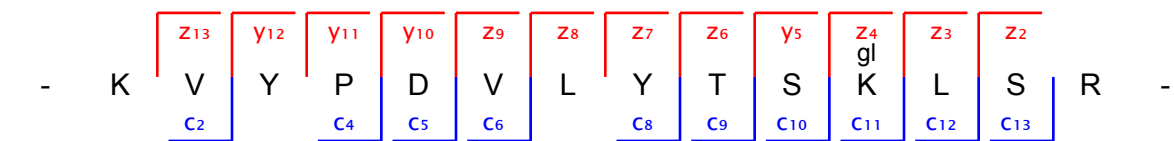
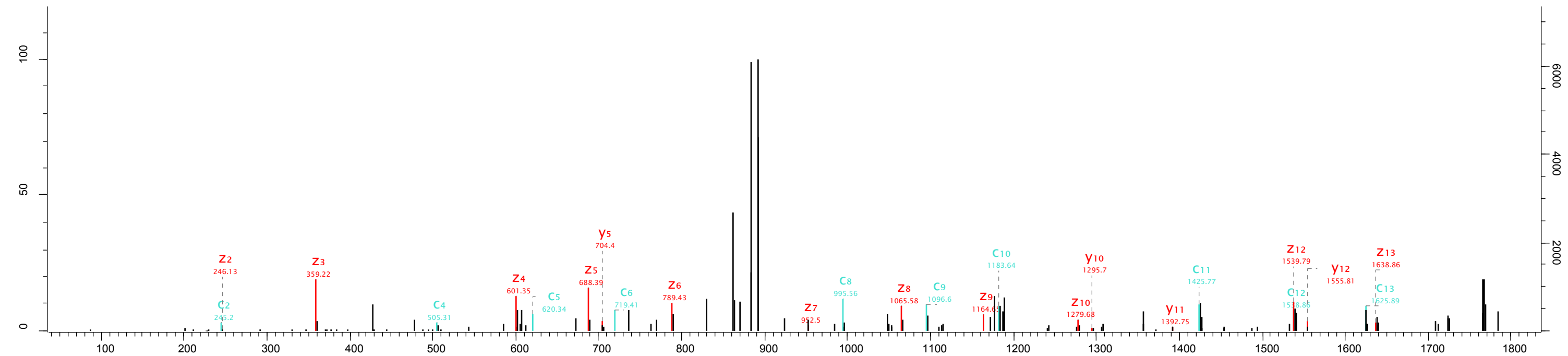


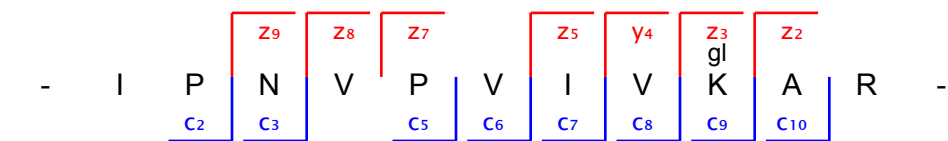
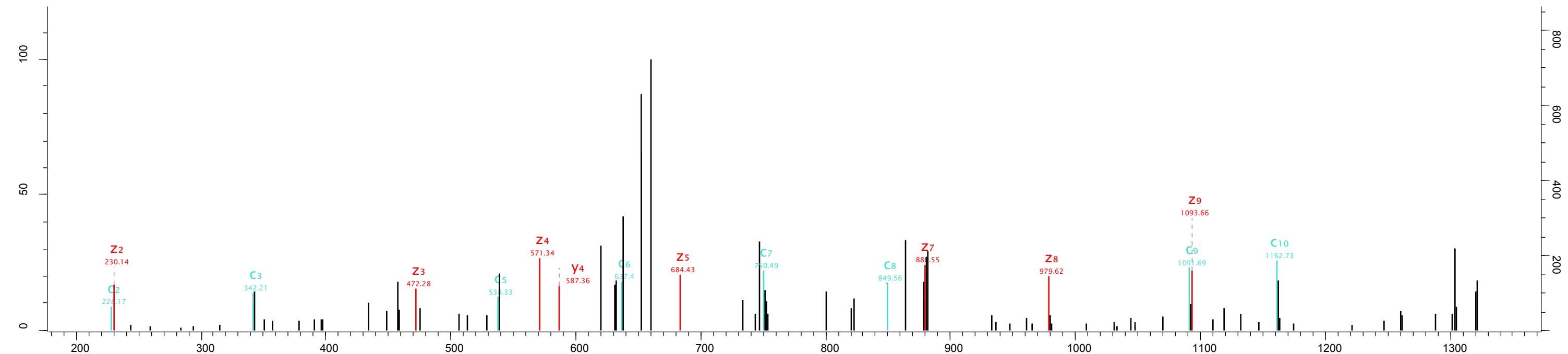


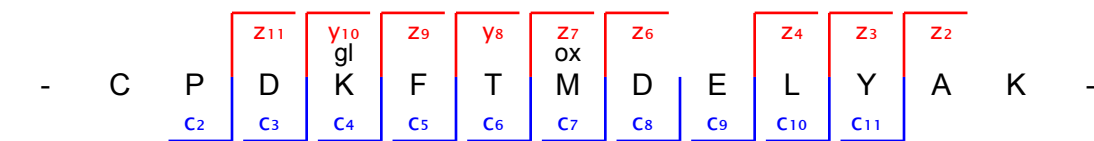
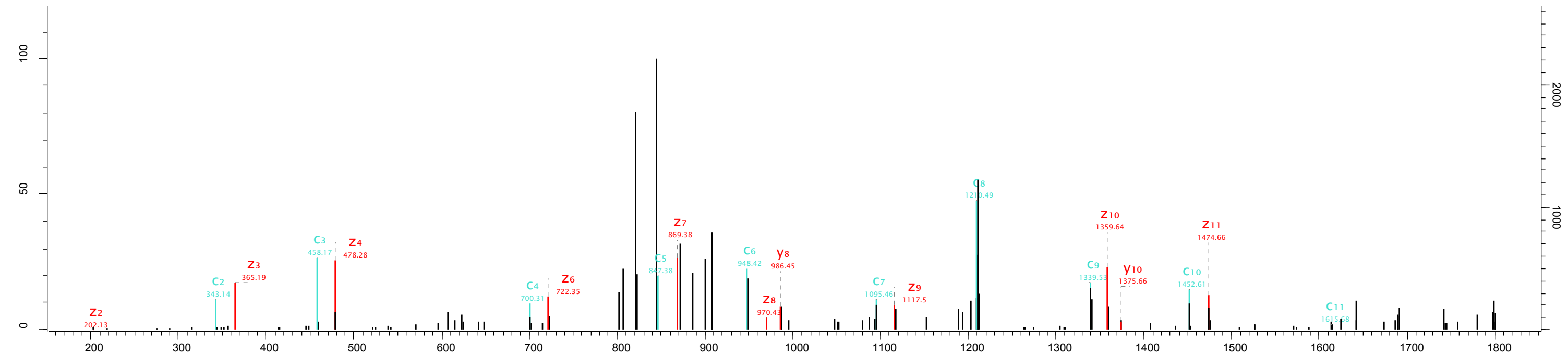


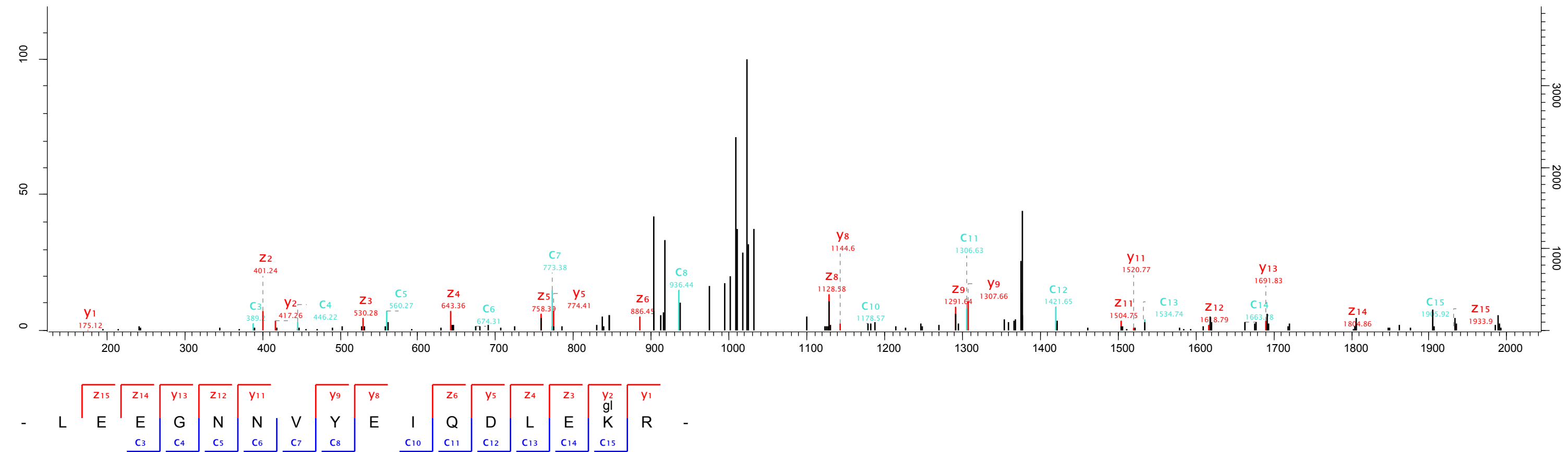


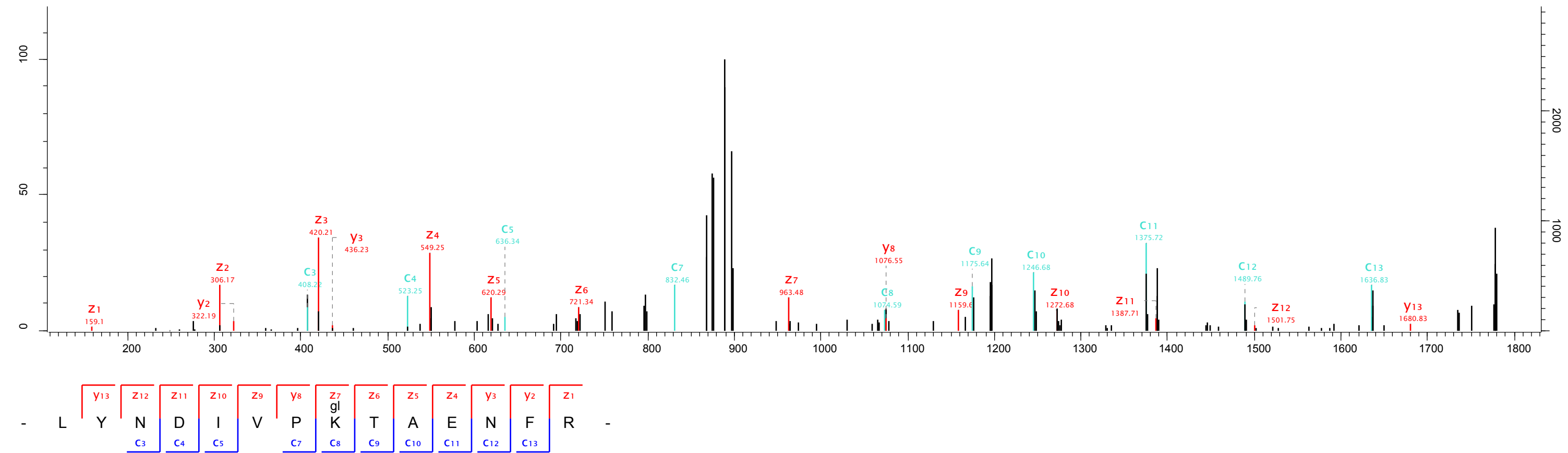


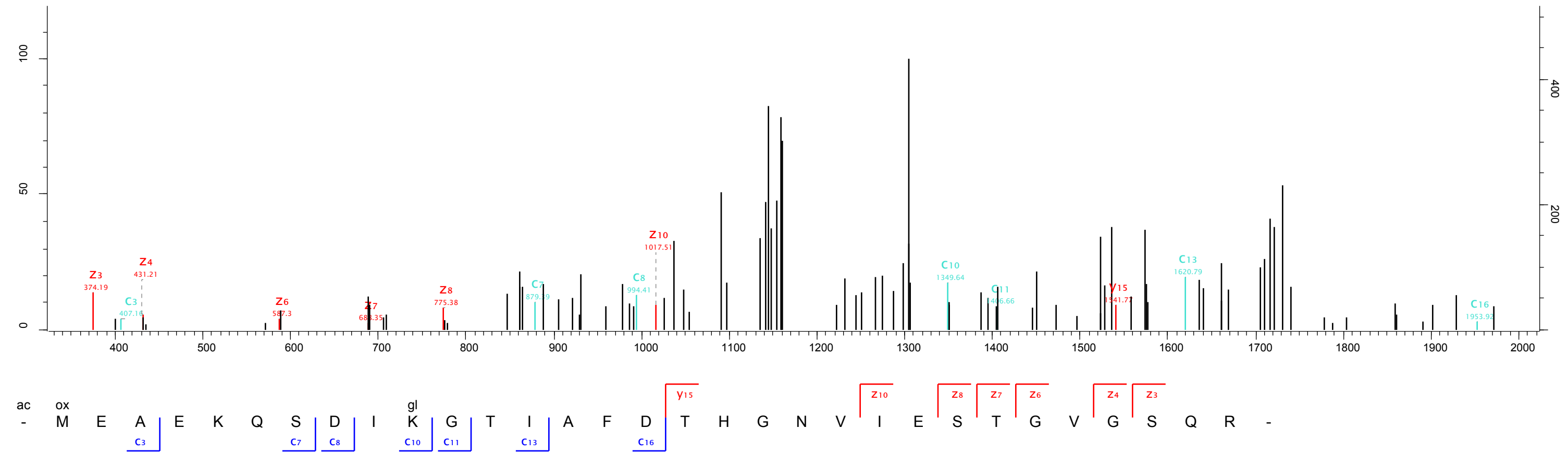


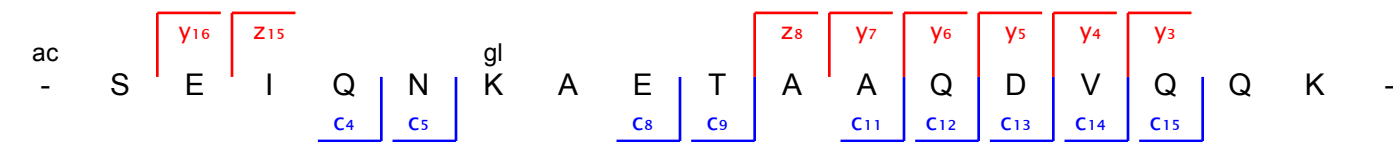
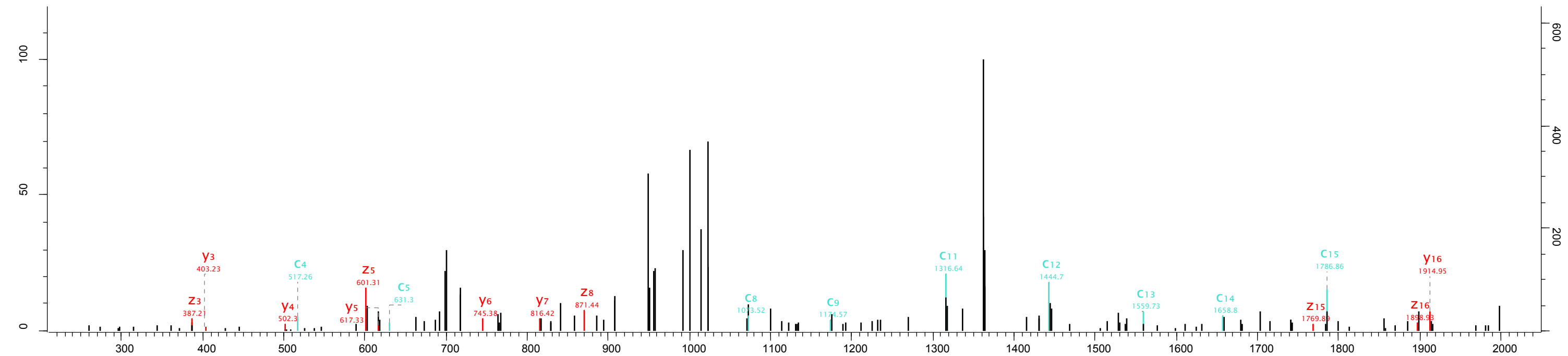


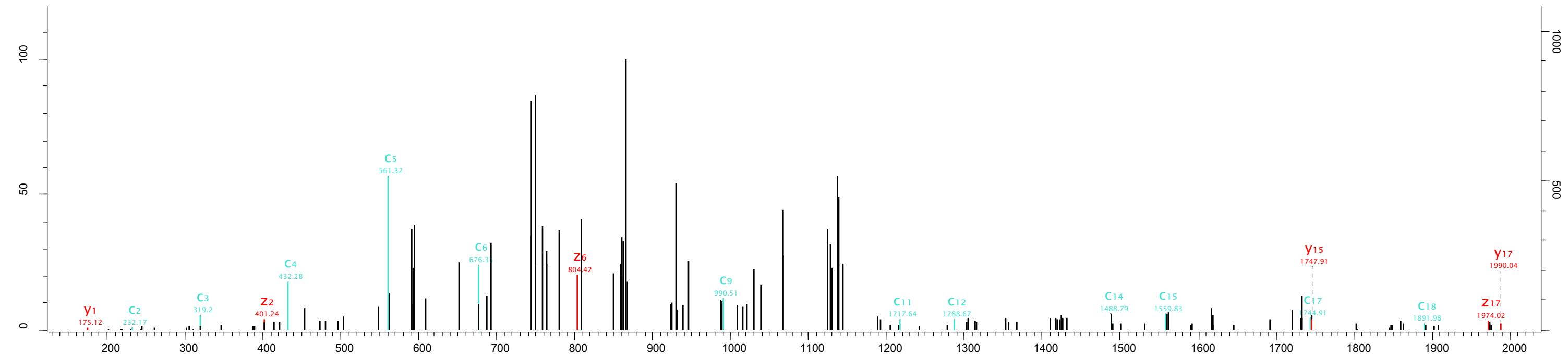












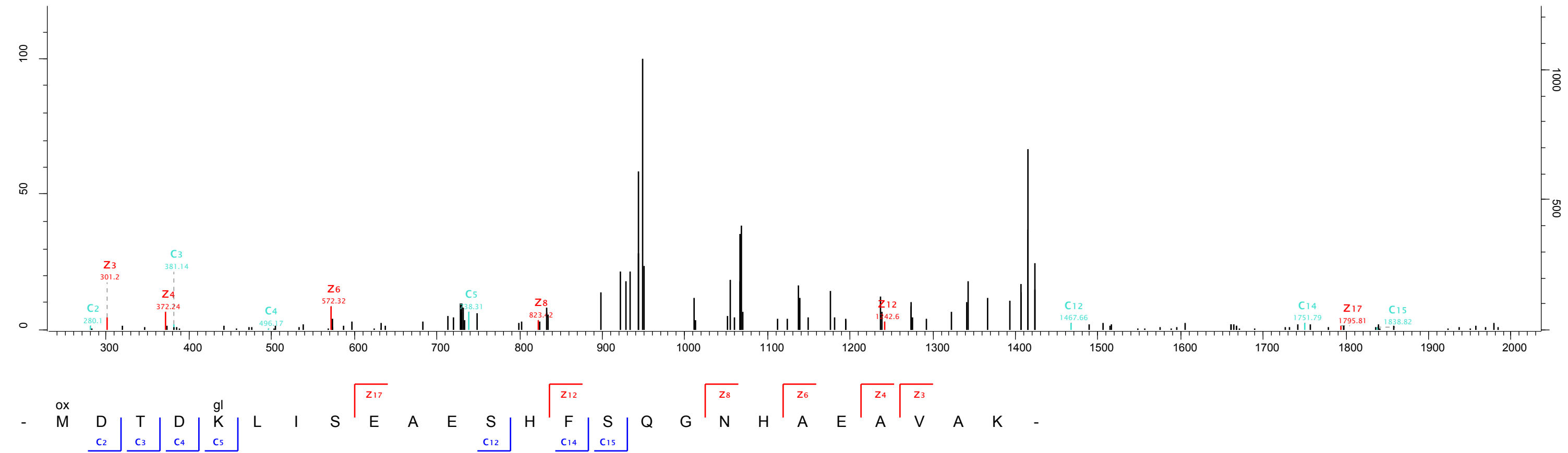
- L T S I E D K A D N L A I S A Q G F K R -

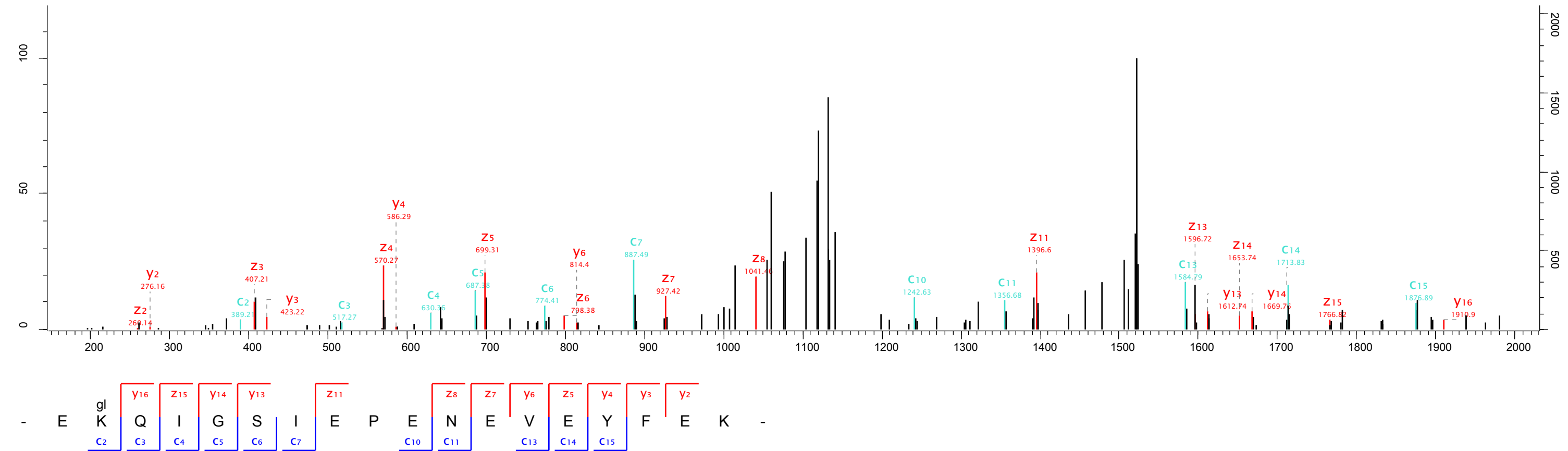
Peptide sequence: L T S I E D K A D N L A I S A Q G F K R

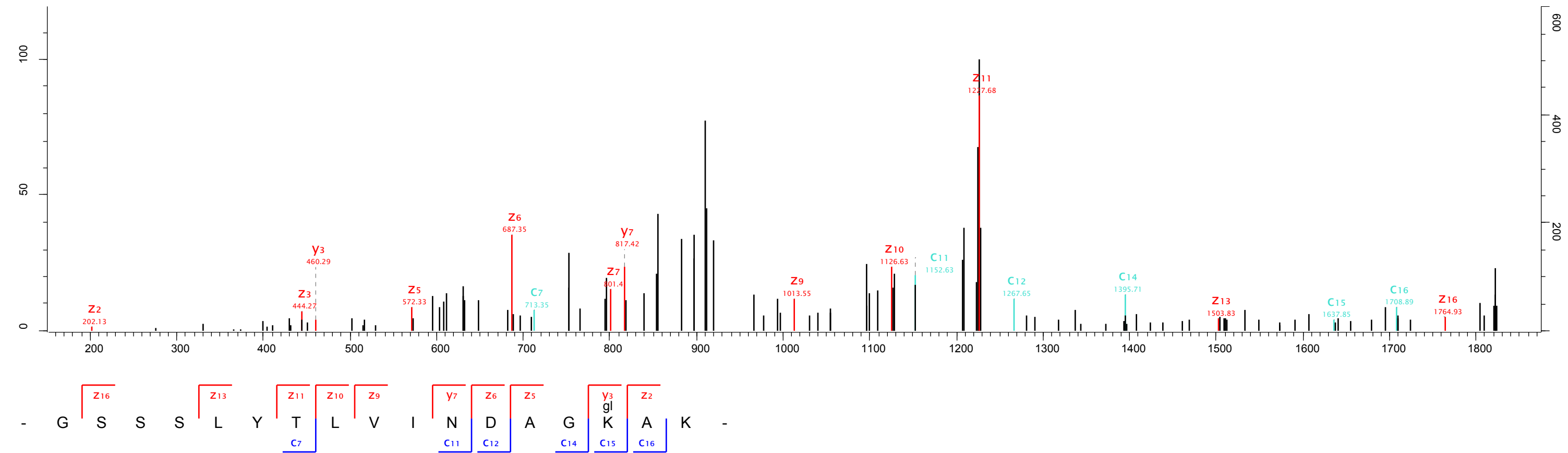
Fragmentation sites (indicated by brackets):

- Y17 (I-E)
- Y15 (E-D)
- Z6 (S-A)
- Z2 (F-K)
- Y1 (K-R)

Charge state: 2+ (indicated by '2' in the label)

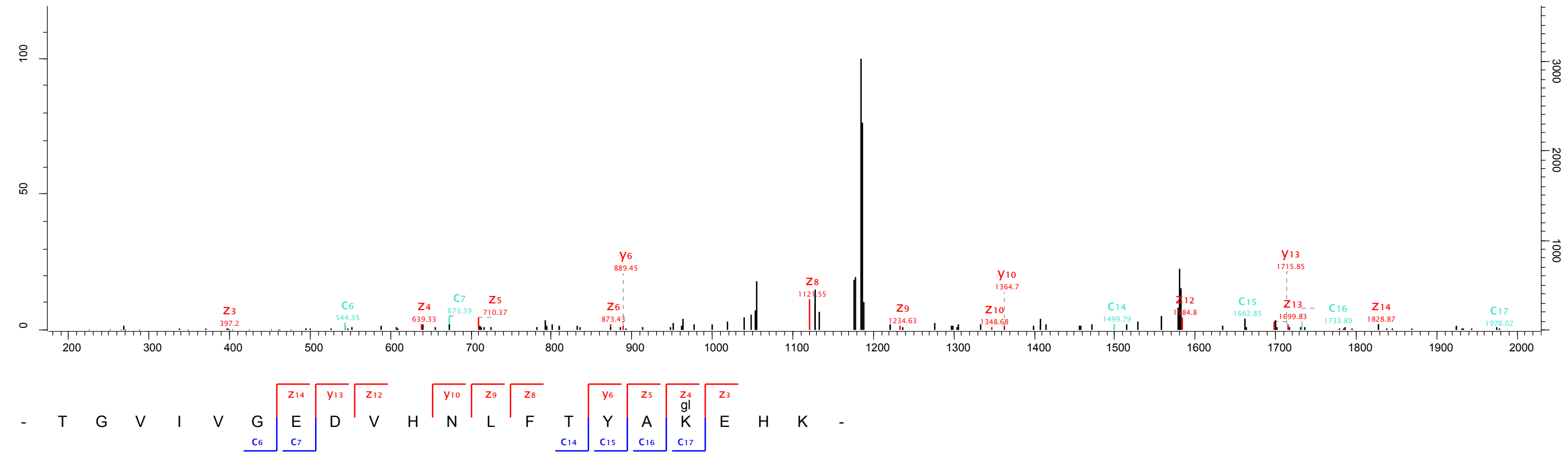






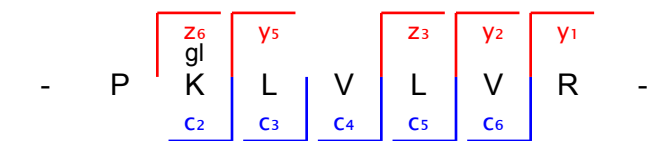
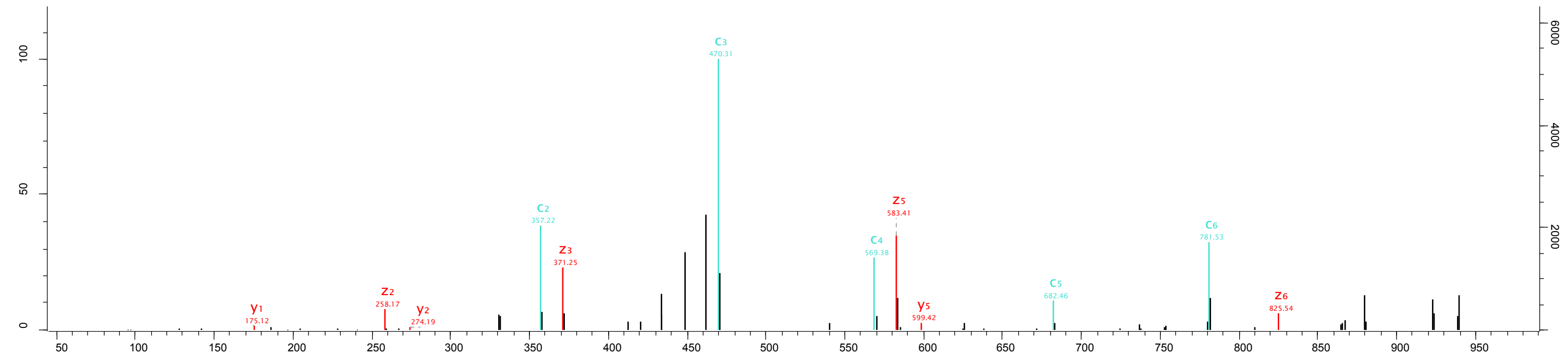
tay_Yeast_Untreated_WCLip_GG_plus3andUp_etd_05August14_02

Scan	Method	Score	m/z
13842	ITMS; ETD	112.5	791.74



tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_B_06August14_05

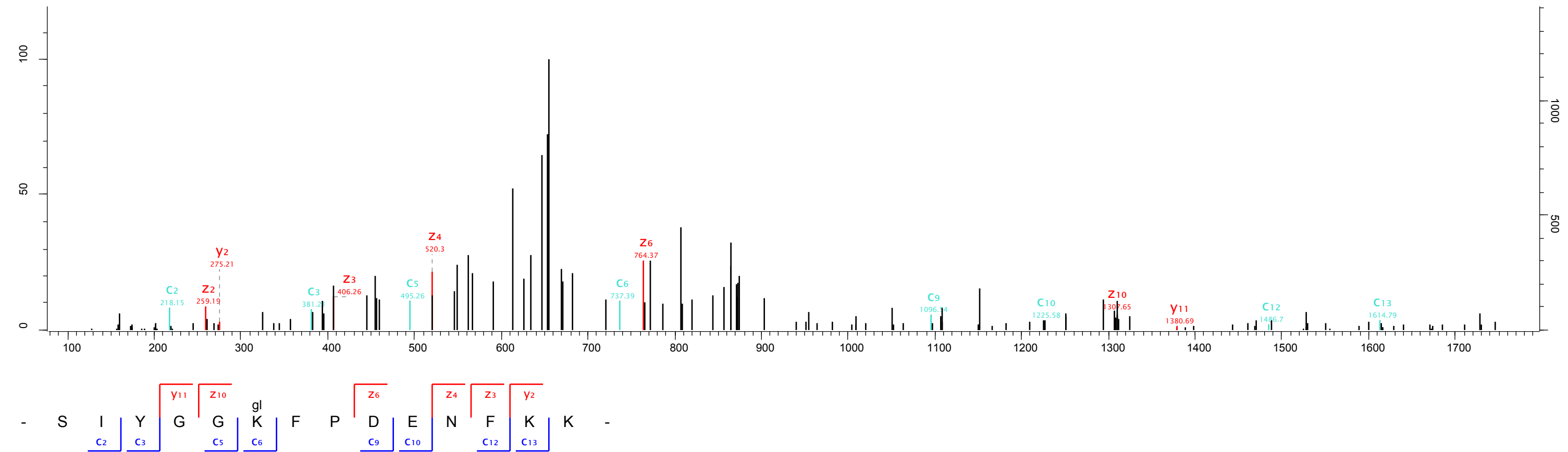
Scan	Method	Score	m/z
5257	ITMS; ETD	178.94	313.54

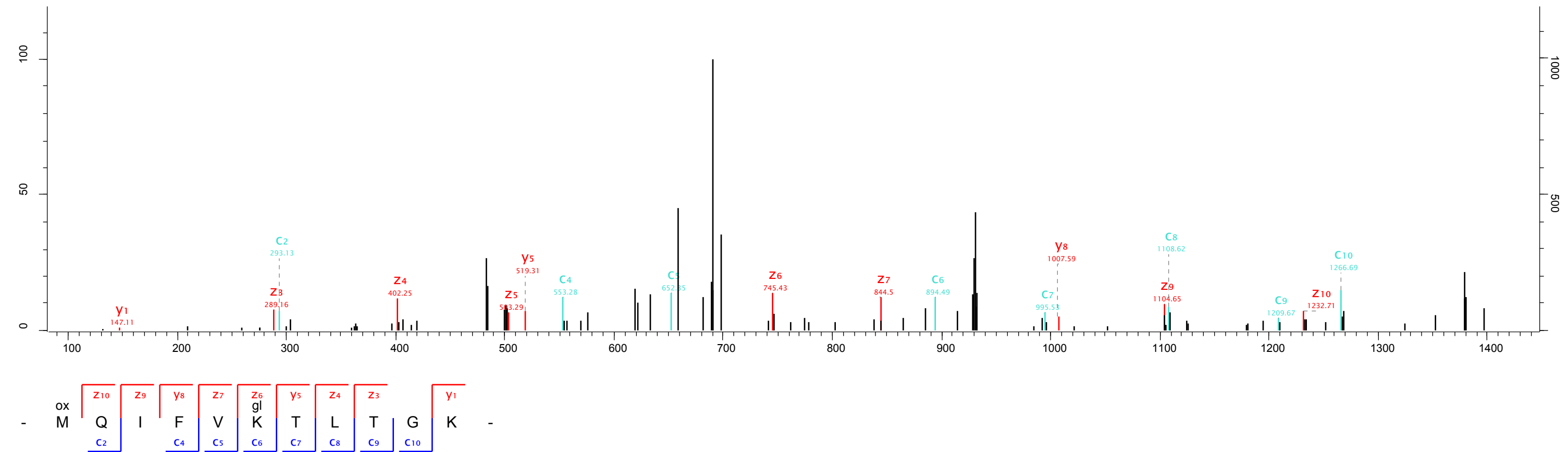


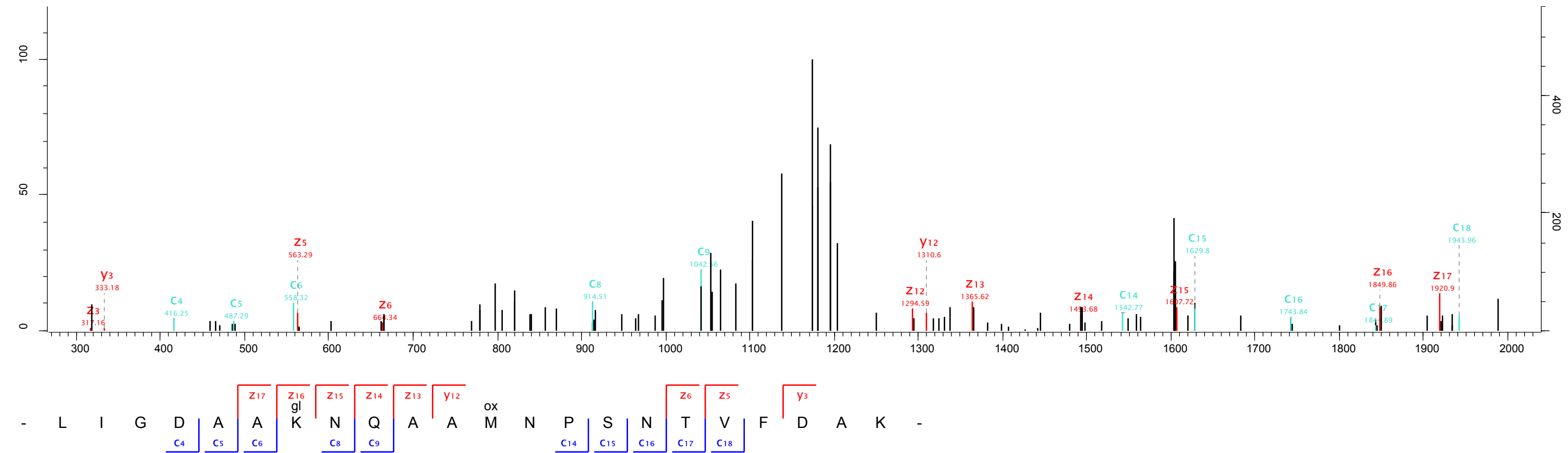
Raw file

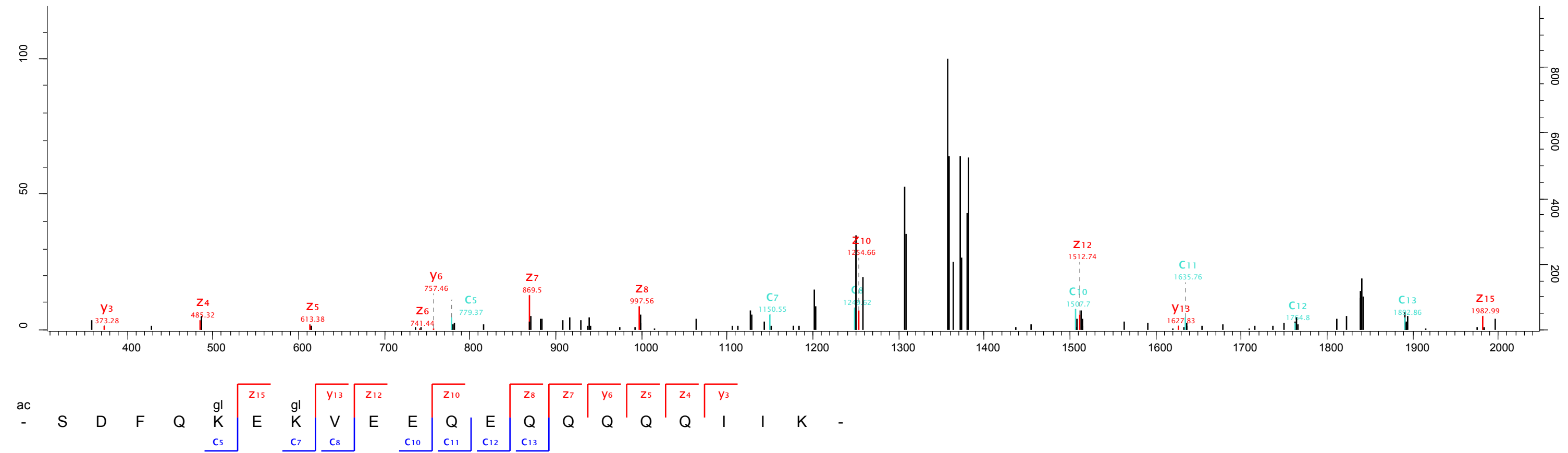
tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_B_06August14_05

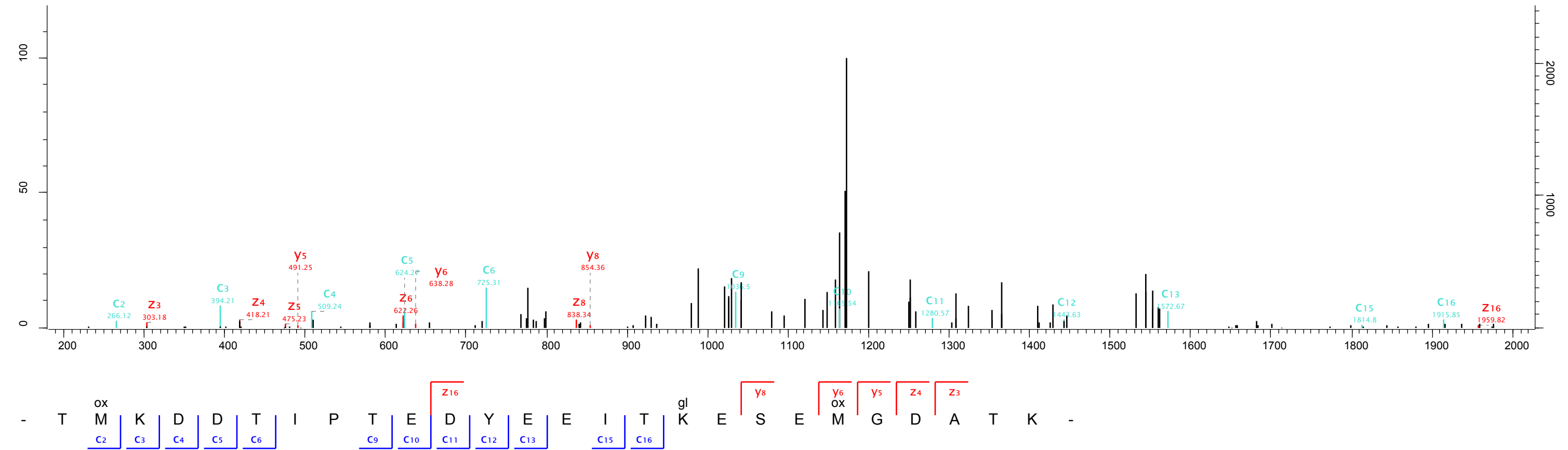
Scan	Method	Score	m/z
7538	ITMS; ETD	106.88	436.97



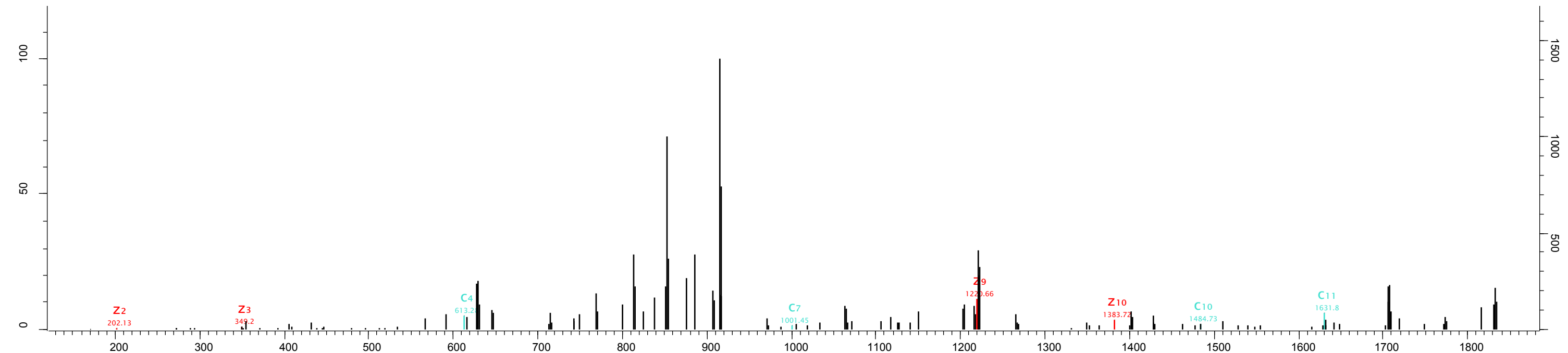






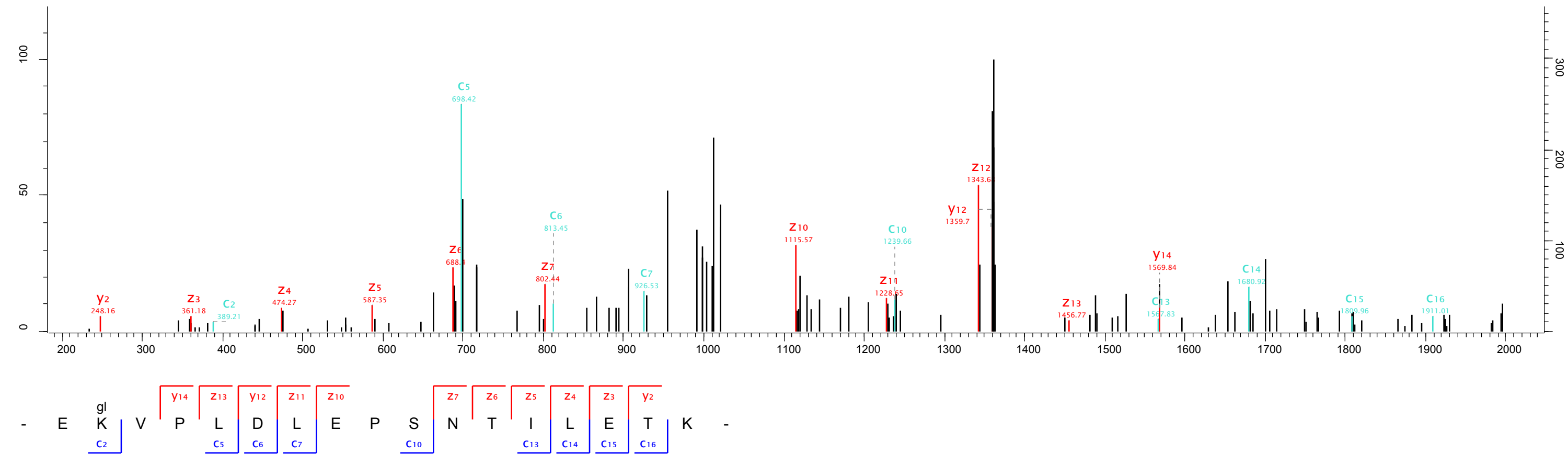


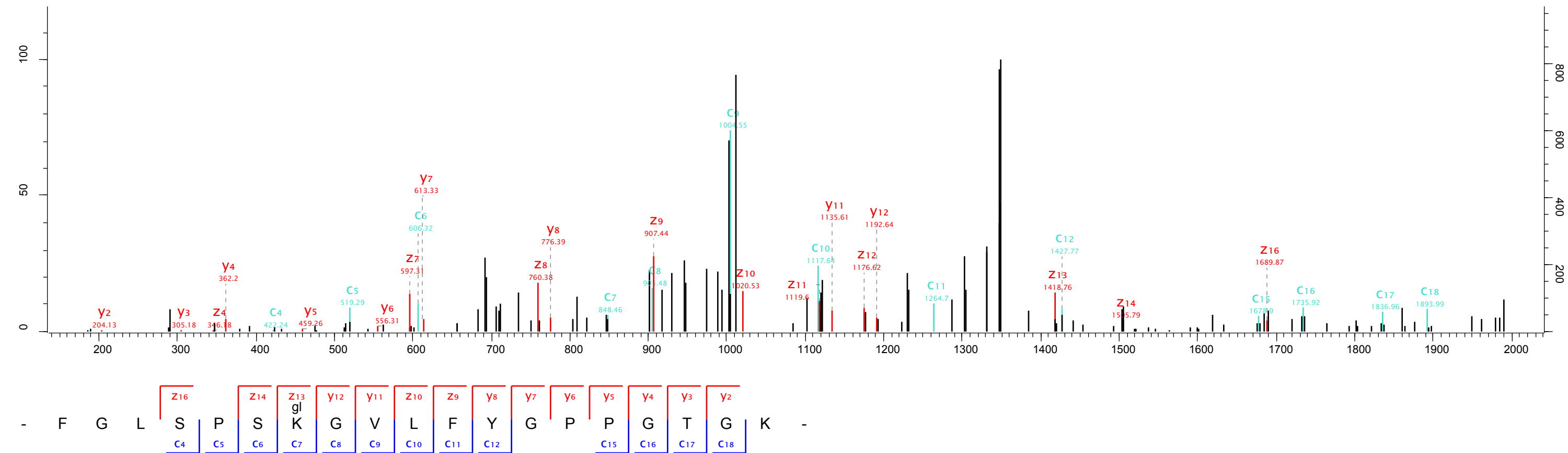
tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_C_06August14_09

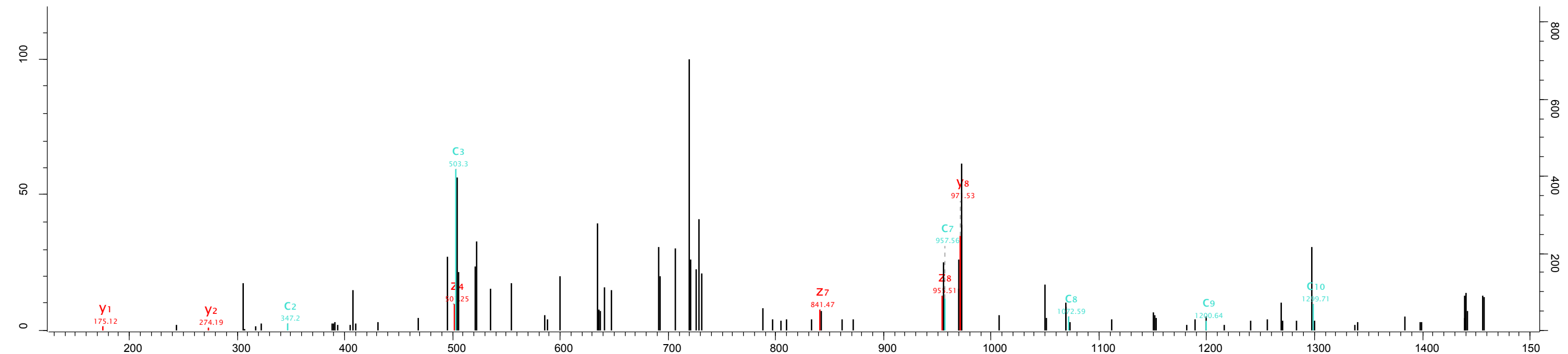


ac ox R S Y M Q I L Q gl K F A K -

Labels: Z10, Z9 ox, Z3, Z2, C4, C7, C10, C11

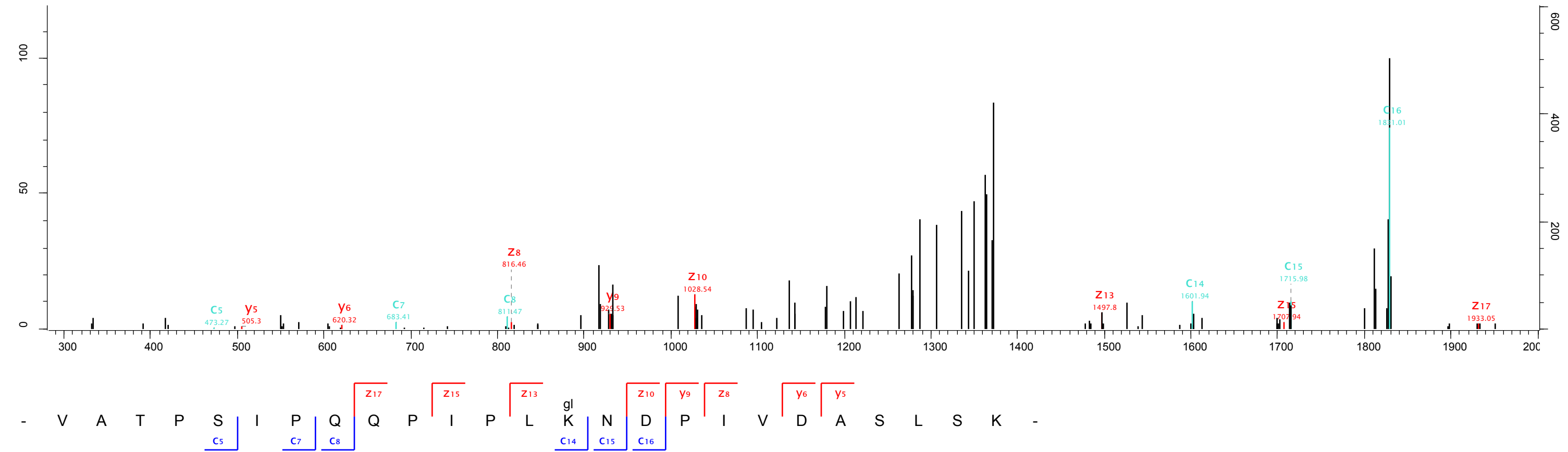


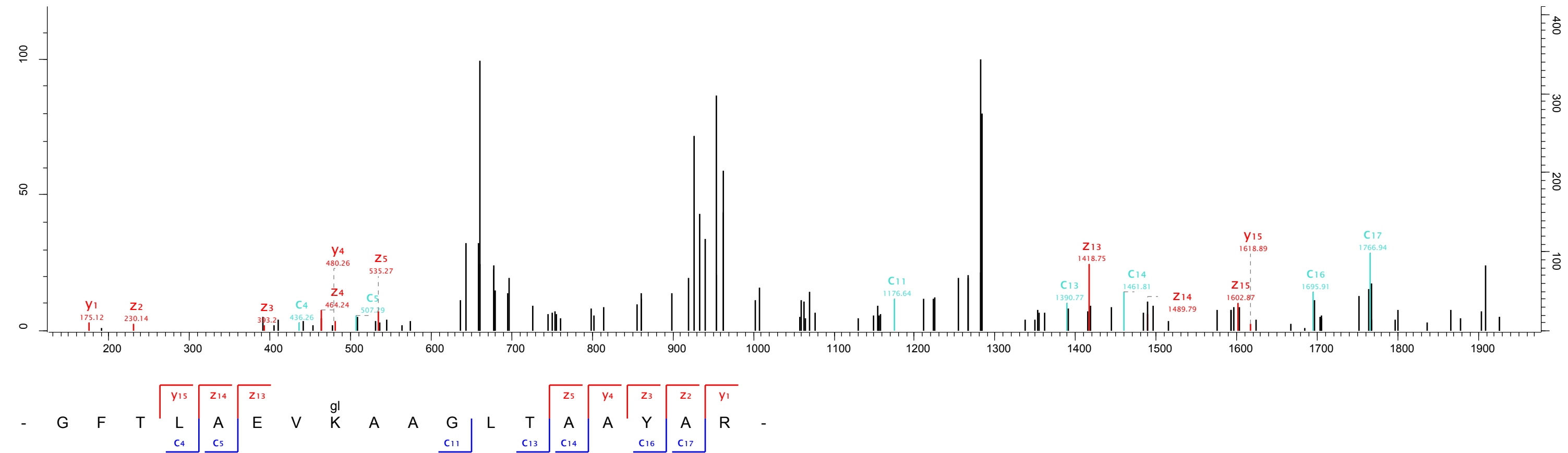




Raw file
tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_C_06August14_09

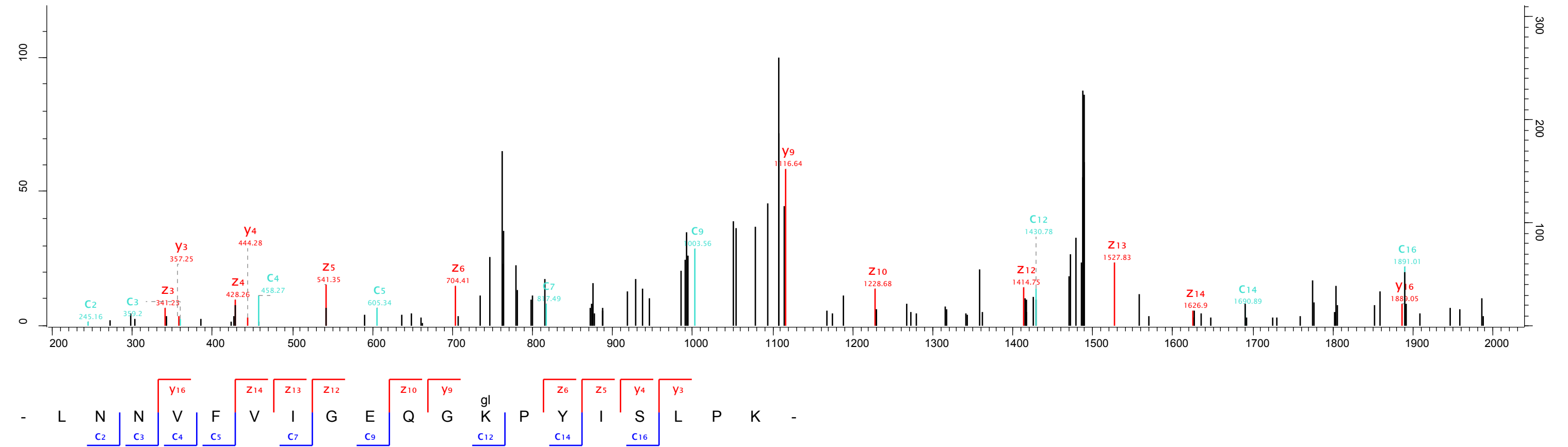
Scan	Method	Score	m/z
15492	ITMS; ETD	63.68	915.51





Raw file
tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_C_06August14_09

Scan	Method	Score	m/z
16154	ITMS; ETD	132.52	744.75



Raw file
tay_Yeast_Untreated_WCLip_GG_plus3andUp_ETD_C_06August14_09

Scan	Method	Score	m/z
8746	ITMS; ETD	54.41	505.23

